

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:27:48 ; Search time 116.174 Seconds  
(without alignments)  
1245.097 Million cell updates/sec

Title: US-10-791-166-2

Perfect score: 1970

Sequence: 1 MLSTSRFRIRNTNSESREV.....GKGKSTGRAPEASLDQKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	374	2 AAR79165	Aar79165 Human mon
2	1970	100.0	374	4 AAG80107	Aag80107 Human CCR
3	1970	100.0	374	6 ABU09083	Abu09083 Human che
4	1970	100.0	374	7 ADD44861	Add44861 Human pro
5	1970	100.0	374	7 ADD44861	Add44861 Human pro
6	1970	100.0	374	7 ADP65146	Adp65146 Human che
7	1970	100.0	374	8 ADO29221	Ado29221 Human GPC
8	1970	100.0	374	8 ADQ67847	Adq67847 Human che
9	1823	92.5	344	5 ABG92881	Abg92881 Class I r
10	1823	92.5	344	6 ABG61655	Abu61655 Human mon
11	1823	92.5	344	7 ADF72129	Adf72129 Human G-P
12	1823	92.5	344	8 ADP66217	Adp66217 Human MCP
13	1727.5	87.7	329	4 AAB46859	Aab46859 Human MCP
14	1727.5	87.7	329	5 ABB81055	Abb81055 Human MCP
15	1727.5	87.7	329	6 ADR16266	Adr16266 Human MCP
16	1651.5	83.8	360	2 AAR79166	Aar79166 Human mon
17	1651.5	83.8	360	2 AAW35833	Aaw35833 Human mon
18	1651.5	83.8	360	4 AAG80108	Aag80108 Human CCR
19	1651.5	83.8	360	4 AAU07614	Aau07614 Human wil
20	1651.5	83.8	360	6 ABP97725	Abp97725 Amino aci
21	1651.5	83.8	360	6 ABP81987	Abp81987 Human C-C
22	1651.5	83.8	360	8 ADM67225	Adm67225 Human adi
23	1651.5	83.8	360	8 ADL82831	Adl82831 Human PRO
24	1650.5	83.8	360	4 AAU07613	Aau07613 Human CCR
25	1645.5	83.5	360	4 ABB56340	Abb56340 Non-endog

26	1589.5	80.7	347	7	ADP56627	Adf56627 Partial h
27	1332.5	67.6	373	8	ADM67224	Adm67224 Murine ad
28	1332.5	67.6	373	8	ADO29222	Ado29222 Mouse GPC
29	1332.5	67.6	373	8	ADP74040	Adp74040 Murine CC
30	1244	63.1	354	8	ADO29228	Ado29228 Mouse GPC
31	1236	62.7	352	4	AAG79089	Aag79089 Amino aci
32	1234	62.7	352	4	AAW54037	Aaw54037 Mouse CC-
33	1230	62.4	354	7	ADD44859	Add44859 Rat Prote
34	1230	62.4	354	7	ADD44863	Add44863 Rat Prote
35	1224	62.1	352	2	AAW27407	Aaw27407 Human CCR
36	1224	62.1	352	2	AAW27123	Aaw27123 Human che
37	1224	62.1	352	2	AAW27125	Aaw27125 Macaque c
38	1224	62.1	352	2	AAW23835	Aaw23835 Human CC
39	1224	62.1	352	2	AAW88232	Aaw88232 HIV-1 co-
40	1224	62.1	352	4	AAE07048	Aae07048 Human G-p
41	1224	62.1	352	4	AAG80111	Aag80111 Human CCR
42	1224	62.1	352	4	AAE04321	Aae04321 Human che
43	1224	62.1	352	4	AAE07039	Aae07039 Human G-p
44	1224	62.1	352	4	AAB46858	Aab46858 Human HDG
45	1224	62.1	352	4	AAB83354	Aab83354 Human CCR

ALIGNMENTS

RESULT 1

AAR79165

ID AAR79165 standard; protein; 374 AA.

XX AAR79165;

AC AAR79165;

XX AAR79165;

DT 25-MAR-2003 (revised)

DT 29-DEC-1995 (first entry)

XX Human monocyte chemoattractant protein-1

DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.

XX Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.

XX Homo sapiens.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..48

FT Domain /label= extracellular

FT Domain 49..70

FT Domain /label= transmembrane

FT Domain 80..700

FT Domain /label= transmembrane

FT Domain 115..136

FT Domain /label= transmembrane

FT Domain 154..178

FT Domain /label= transmembrane

FT Domain 204..231

FT Domain /label= transmembrane

FT Domain 244..268

FT Domain /label= transmembrane

FT Domain 295..313

FT Domain /label= transmembrane

FT Region 314..375

FT Region /label= carboxyl tail

XX WO9519436-A1.

PN 20-JUL-1995.

XX 11-JAN-1995; 95WO-US000476.

XX 13-JAN-1994; 94US-00182962.

PR (REGC ) UNIV CALIFORNIA.

PA Charo I, Coughlin S;

XX WPI; 1995-263866/34.

DR N-PSDB; AAQ96297.  
 XX DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.  
 PT for identifying antagonists and for treating diseases characterised by  
 PT monocytic infiltrates.  
 XX  
 XX Claim 2; Fig 1; 84pp; English.  
 XX  
 CC To identify and clone new members of the chemokine receptor gene family,  
 CC degenerate oligo primers were designed corresp. to the conserved  
 CC sequences R79167 in the second and R79168 in the third transmembrane  
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the  
 CC HUMSTRS orphan receptor (GenBank Accession #M99293). The degenerate oligo  
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and  
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers  
 CC yielded a number of PCR products. One cDNA appeared to encode a novel  
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA  
 CC library was constructed in pPROG and probed with the PCR product. A 2.1  
 CC kb cDNA clone was obtained. Analysis of additional clones in the MM6 cDNA  
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA  
 CC sequence first obtained from the 5' UTR through the putative seventh  
 CC transmembrane domain but contained a different cytoplasmic tail. The  
 CC second sequence appears to represent alternative splicing of the carboxyl  
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-  
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-  
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.  
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct FN  
 CC field.)  
 XX  
 XX Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 2; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLPPLYSLVFIFGVGN 60  
 DB 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLPPLYSLVFIFGVGN 60  
 QY 61 MLVVLILNCKKLCITDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120  
 DB 61 MLVVLILNCKKLCITDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120  
 QY 121 HIGVFGGIFPIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
 DB 121 HIGVFGGIFPIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
 QY 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240  
 DB 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLFWTPPNVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 DB 241 AVRVIPTIMIVYFLFWTPPNVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 QY 301 NPITVAVGKPSLFHIALGCRITAPLQKPCVCGPGRVPCKNVKTVTQGLDGRGKSI 360  
 DB 301 NPITVAVGKPSLFHIALGCRITAPLQKPCVCGPGRVPCKNVKTVTQGLDGRGKSI 360  
 QY 361 GRAPEASLQDKEGA 374  
 DB 361 GRAPEASLQDKEGA 374

RESULT 2  
 AAG80107  
 ID AAG80107 standard; protein; 374 AA.  
 XX  
 XX AAG80107;  
 AC  
 XX 17-JAN-2002 (first entry)  
 DT  
 XX Human CCR2a protein.  
 DE

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
 KW antirheumatic; antiarthritic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200172830-A2.  
 XX  
 XX 04-OCT-2001.  
 XX  
 XX 02-APR-2001; 2001WO-EP003708.  
 XX  
 XX 31-MAR-2000; 2000DE-01016013.  
 XX  
 XX (IPFP-) IPF PHARM GMBH.  
 XX (FORS/) FORSSMANN U.  
 XX  
 XX Forsmann W, Adermann K, Heitland A, Spodsberg N;  
 XX WPI; 2001-626256/72.  
 XX  
 XX Diagnostic agent containing two or more receptor-specific ligands, useful  
 XX for detecting tumors, inflammation etc., also therapeutic use of ligand  
 XX inhibitors.  
 XX  
 XX Disclosure; Page 9; 26pp; German.  
 XX  
 CC This invention describes a novel diagnostic agent (A) comprising at least  
 CC two different ligands (I) for receptors (II) that are implicated in  
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal  
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.  
 CC Also inhibitors of (I) are used therapeutically against tumors (and their  
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel  
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
 CC endocrine, motor or urogenital systems or skin are affected, and bone  
 CC marrow diseases. The products of the invention are chemokine derivatives  
 CC which have cytostatic, antiinflammatory, antiasthmatic,  
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.  
 CC Chemokines act on specific tumor and inflammatory cells through a  
 CC constellation of chemokine receptors (CR), which control migration and  
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine  
 CC fragments used to illustrate the method of the invention  
 XX  
 XX Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 4; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLPPLYSLVFIFGVGN 60  
 DB 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLPPLYSLVFIFGVGN 60  
 QY 61 MLVVLILNCKKLCITDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120  
 DB 61 MLVVLILNCKKLCITDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120  
 QY 121 HIGVFGGIFPIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
 DB 121 HIGVFGGIFPIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
 QY 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240  
 DB 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLFWTPPNVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 DB 241 AVRVIPTIMIVYFLFWTPPNVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCI 300

QY 301 NPIIYAFVGEKPSLPHIALGCRIPALQKPVCGPGVVRPGKVKVTTQGLLDGRGKSI 360  
 DB 301 NPIIYAFVGEKPSLPHIALGCRIPALQKPVCGPGVVRPGKVKVTTQGLLDGRGKSI 360  
 QY 361 GRAPEASLQDKEGA 374  
 DB 361 GRAPEASLQDKEGA 374  
 RESULT 3  
 ABU09083  
 ID ABU09083 standard; protein; 374 AA.  
 XX  
 AC ABU09083;  
 XX  
 DT 23-JUL-2003 (first entry)  
 XX  
 DE Human chemokine receptor-2 (CCR-2) polypeptide.  
 XX  
 KW Human; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor;  
 KW MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma;  
 KW monocyte/dendritic cell receptor for chemokine; inflammatory condition;  
 KW abnormal physiology; abnormal proliferation; degeneration; atrophy;  
 KW antiinflammatory; antiasthmatic; cytostatic; chemokine receptor-2; CCR-2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003018167-A1.  
 XX  
 PD 23-JAN-2003.  
 XX  
 PF 03-JAN-2002; 2002US-00039659.  
 XX  
 PR 05-JUL-1996; 96US-0021664P.  
 PR 11-OCT-1996; 96US-0028329P.  
 PR 04-JUN-1997; 97US-0048593P.  
 PR 03-JUL-1997; 97US-00887977.  
 XX  
 (SCHE ) SCHERING CORP.  
 PA  
 PI Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;  
 XX  
 WPI; 2003-416900/39.  
 XX  
 DR New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful  
 PT for treating conditions associated with abnormal physiology or  
 PT development, including inflammatory conditions (e.g. asthma), and  
 PT abnormal proliferation.  
 XX  
 PS Disclosure; Page 9-10; 54pp; English.  
 XX  
 CC The invention relates to nucleic acids encoding the chemokines TECK, MIP-  
 CC 3alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are  
 CC useful in isolating DNA clones encoding the chemokines, for generating  
 CC antibodies, and for predicting oligonucleotides for screening a library  
 CC to isolate species variants. A nucleic acid encoding a chemokine  
 CC polypeptide can be used to identify genes, mRNA and cDNA species which  
 CC encode related or homologous ligands, as well as DNA encoding homologous  
 CC proteins from different species. The chemokines and antibodies which bind  
 CC to the polypeptides are useful in the treatment of conditions associated  
 CC with abnormal physiology or development, including inflammatory  
 CC conditions such as asthma, abnormal proliferation, regeneration,  
 CC degeneration and atrophy. This sequence represents the human chemokine  
 CC receptor-2 (CCR-2) polypeptide, used in the scope of the invention  
 XX  
 SQ Sequence 374 AA;  
 Query Match 100.0%; Score 1970; DB 6; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIFFGVGN 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIFFGVGN 60  
 QY 61 MLVVLILINCKLCKLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 61 MLVVLILINCKLCKLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 HIGYFGGIPFIILLITDRYLAI VHAVFALKARTVTFGVTSVITLWVAFASVPGIIFTK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 121 HIGYFGGIPFIILLITDRYLAI VHAVFALKARTVTFGVTSVITLWVAFASVPGIIFTK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 CQKEDSVYVCGPYFPRGMNFHTIMENILGLVPLLIWVICYSGILKTLRCRNEKRRH 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 181 CQKEDSVYVCGPYFPRGMNFHTIMENILGLVPLLIWVICYSGILKTLRCRNEKRRH 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 241 AVRVIPTIMIVYELFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 241 AVRVIPTIMIVYELFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 301 NPIIYAFVGEKPSLPHIALGCRIPALQKPVCGPGVVRPGKVKVTTQGLLDGRGKSI 360  
 DB 301 NPIIYAFVGEKPSLPHIALGCRIPALQKPVCGPGVVRPGKVKVTTQGLLDGRGKSI 360  
 QY 361 GRAPEASLQDKEGA 374  
 DB 361 GRAPEASLQDKEGA 374  
 RESULT 4  
 ADD44861  
 ID ADD44861 standard; protein; 374 AA.  
 XX  
 AC ADD44861;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human Protein P41597, SEQ ID NO 10292.  
 XX  
 KW Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003016475-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX  
 WPI; 2003-268312/26.  
 DR GENBANK; P41597.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.  
 XX  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. Gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 374 AA;  
 Query Match 100.0%; Score 1970; DB 7; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLSLVIFGFGVGN 60  
 DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLSLVIFGFGVGN 60  
 QY 61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
 DB 61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
 QY 121 HIGYFGGIFPIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
 DB 121 HIGYFGGIFPIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
 QY 181 CQKEDSVYVCGPYFPRGWNFNHTIMRNILGLVPLLMVICYSGILKTLRCKNEKKRHR 240  
 DB 181 CQKEDSVYVCGPYFPRGWNFNHTIMRNILGLVPLLMVICYSGILKTLRCKNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
 DB 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGPGVVRPGKNVKTQTQGLDGRGKSI 360  
 DB 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGPGVVRPGKNVKTQTQGLDGRGKSI 360  
 QY 361 GRAPEASLQDKEGA 374  
 DB 361 GRAPEASLQDKEGA 374

RESULT 5  
 ADD44865  
 ID ADD44865 standard; protein; 374 AA.  
 XX  
 AC ADD44865;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human Protein P41597, SEQ ID NO 10296.  
 XX  
 KW Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003016475-A2.

XX PD 27-FEB-2003.  
 XX PF 14-AUG-2002; 2002WO-US025765.  
 XX PR 14-AUG-2001; 2001US-0312147P.  
 XX PR 01-NOV-2001; 2001US-0346382P.  
 XX PR 26-NOV-2001; 2001US-0333347P.  
 XX PA (GEO) GEN HOSPITAL CORP.  
 XX PA (FARB) BAYER AG.  
 XX PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI; 2003-268312/26.  
 XX DR GENBANK; P41597.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. Gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 374 AA;  
 Query Match 100.0%; Score 1970; DB 7; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLSLVIFGFGVGN 60  
 DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLSLVIFGFGVGN 60  
 QY 61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
 DB 61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
 QY 121 HIGYFGGIFPIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
 DB 121 HIGYFGGIFPIILLTIDRYLAIHVAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
 QY 181 CQKEDSVYVCGPYFPRGWNFNHTIMRNILGLVPLLMVICYSGILKTLRCKNEKKRHR 240  
 DB 181 CQKEDSVYVCGPYFPRGWNFNHTIMRNILGLVPLLMVICYSGILKTLRCKNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300

Db 241 AVRIIVTITVYFLFWTPYNNVILLNTFQBFGLSNCESTSDQATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPCVCGPGVVRPGKVKVTTQGLDGRGKSI 360  
 Db 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPCVCGPGVVRPGKVKVTTQGLDGRGKSI 360  
 QY 361 GRAPEASLQDKEGA 374  
 Db 361 GRAPEASLQDKEGA 374  
 RESULT 6  
 ID ADP65146 standard; protein; 374 AA.  
 XX AC ADP65146;  
 XX 12-AUG-2004 (first entry)  
 DE Human chemokine (C-C motif) receptor 2, isoform A, chemokine (C-C).  
 XX autoimmune disease; arthritis; gene expression analysis;  
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; anti-rheumatic;  
 KW antiarthritis; osteopathic; antigout; antiinflammatory; dermatological;  
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;  
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
 KW immune; human.  
 XX Homo sapiens.  
 OS  
 XX WO2003072827-A1.  
 XX 04-SEP-2003.  
 XX 31-OCT-2002; 2002WO-US035433.  
 XX 31-OCT-2001; 2001US-0336220P.  
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX Hirsch R, Thorton SL;  
 WPI; 2003-712740/67.  
 DR GENBANK; NP\_000638.  
 PT Diagnosing and analyzing autoimmune disease using gene expression  
 PT profiles and microarray technology, useful for diagnosing and treating  
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
 PT gout.  
 XX Disclosure; Page; 56pp; English.  
 XX The invention relates to a novel method for diagnosing and analysing  
 CC autoimmune disease or arthritides. The method comprises obtaining a  
 CC patient sample containing mRNA, analysing gene expression using the mRNA  
 CC that results in a gene expression signature of the mRNA, and using that  
 CC gene expression signature to diagnose or analyse the autoimmune disease  
 CC or arthritides in the patient, where gene expression of at least 60% of  
 CC the genes correlates with that of the gene signature. The invention  
 CC further comprises: a treatment of rheumatoid arthritis; identification of  
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal  
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal;  
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
 CC efficacy of a candidate drug in vitro for the treatment of collagen-  
 CC induced arthritis; and reducing the symptoms associated with collagen-  
 CC induced arthritis. The compositions of the invention have the following  
 CC activities: immunosuppressive, anti-rheumatic, antiarthritis, osteopathic,  
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
 CC methods and compositions of the present invention are useful for  
 CC diagnosing and treating autoimmune disease or arthritides, such as  
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,

CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 CC immune disease caused by an infectious agent. This sequence represents a  
 CC protein sequence relating to the genes used in the analysis and treatment  
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown  
 CC in the specification. It has been supplied in an electronic format from  
 CC WIPO.  
 XX  
 SQ Sequence 374 AA;  
 Query Match 100.0%; Score 1970; DB 7; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRSFTRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLLPPLYSLVFIFGVGN 60  
 Db 1 MLSTSRSFTRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLLPPLYSLVFIFGVGN 60  
 QY 61 MLVVLILINCKKLCCLTDIYLLNLAI SDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 Db 61 MLVVLILINCKKLCCLTDIYLLNLAI SDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 QY 121 HIGYFGGIFPIILLTIDRYLAI VHAVFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180  
 Db 121 HIGYFGGIFPIILLTIDRYLAI VHAVFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180  
 QY 181 CQKEDSVYVCGPYPPGWNFNFTIMRNILGLVPLLMVJCYSGILKTLRCRNEKKRHR 240  
 Db 181 CQKEDSVYVCGPYPPGWNFNFTIMRNILGLVPLLMVJCYSGILKTLRCRNEKKRHR 240  
 QY 241 AVRVIETIMIVYFLWTPYNNVILLNTFQBFGLSNCESTSDQATQVTTGLMTHCCI 300  
 Db 241 AVRVIETIMIVYFLWTPYNNVILLNTFQBFGLSNCESTSDQATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPCVCGPGVVRPGKVKVTTQGLDGRGKSI 360  
 Db 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPCVCGPGVVRPGKVKVTTQGLDGRGKSI 360  
 QY 361 GRAPEASLQDKEGA 374  
 Db 361 GRAPEASLQDKEGA 374  
 RESULT 7  
 ID ADO29221 standard; protein; 374 AA.  
 XX ADO29221;  
 AC ADO29221;  
 XX 29-JUL-2004 (first entry)  
 DT Human GPCR CCR2, SEQ ID NO:322.  
 XX  
 XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;  
 KW cytotatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antiarrhoeic; antidiabetic;  
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;  
 KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 KW receptor.  
 XX Homo sapiens.  
 OS  
 XX WO2004040000-A2.  
 XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.  
 XX 09-SEP-2002; 2002US-0409303P.  
 PR 09-APR-2003; 2003US-0461329P.  
 XX (PRIM-) PRIMAL INC.  
 PA Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li P;  
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;  
 XX N-PSDB; ADO29829.  
 DR WPI; 2004-390329/36.  
 DR N-PSDB; ADO29829.  
 XX Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX Claim 151; SEQ ID NO 322; 542pp; English.  
 XX The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridize to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
 CC invention. Note: The full sequence data for this patent did not form part  
 CC of the printed specification; those sequences not shown were obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 374 AA;  
 Query Match 100.0%; Score 1970; DB 8; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRSRFIRNTNSESSEVTFDFDYDGAPCHKFDVKQIGAGLLPPLYSLVIFGFGVN 60  
 DB 1 MLSTSRSRFIRNTNSESSEVTFDFDYDGAPCHKFDVKQIGAGLLPPLYSLVIFGFGVN 60  
 QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWHAASAANWVFGNACMLFTGLY 120  
 DB 61 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWHAASAANWVFGNACMLFTGLY 120  
 QY 121 HIGVFGIFPIILLITDIYLAIVHAVFALKARTVFGVTSVITLWVAVFASVPGIIFTK 180  
 DB 121 HIGVFGIFPIILLITDIYLAIVHAVFALKARTVFGVTSVITLWVAVFASVPGIIFTK 180  
 QY 181 CQKEDSVYVCGPYFPRGWNFNHTIMRNILGLVLLIMVICYSGILKTLRCRNEKKRHR 240

DB 181 CQKEDSVYVCGPYFPRGWNFNHTIMRNILGLVLLIMVICYSGILKTLRCRNEKKRHR 240  
 QY 241 AVRVIETIMIVVFLFWTPYNIIVILLNTFOEFFGLSNCESTSQDQATQVTTETLGMTHCCI 300  
 DB 241 AVRVIETIMIVVFLFWTPYNIIVILLNTFOEFFGLSNCESTSQDQATQVTTETLGMTHCCI 300  
 QY 301 NPIIYAFVGEKFRSLFPHIALGCRAPLQKPVCGGVRPGKKNVKTTOGLLDGRGKSKI 360  
 DB 301 NPIIYAFVGEKFRSLFPHIALGCRAPLQKPVCGGVRPGKKNVKTTOGLLDGRGKSKI 360  
 QY 361 GRAPEASLQDKEGA 374  
 DB 361 GRAPEASLQDKEGA 374  
 RESULT 8  
 ADQ67847  
 ID ADQ67847 standard; protein; 374 AA.  
 XX AC ADQ67847;  
 XX DT 07-OCT-2004 (first entry)  
 DE Human chemokine receptor CCR-2.  
 XX KW Human; receptor; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;  
 KW chemokine receptor; DCCR; dendritic cell receptor for chemokine; M/DCCR;  
 KW Monocyte/dendritic cell receptor for chemokine; abnormal physiology;  
 KW development; inflammatory condition; asthma.  
 XX OS Homo sapiens.  
 PN US2004137578-A1.  
 PD 15-JUL-2004.  
 XX 09-JAN-2004; 2004US-00754071.  
 XX 05-JUL-1996; 96US-0021664P.  
 PR 11-OCT-1996; 96US-0028329P.  
 PR 04-JUN-1997; 97US-0048593P.  
 PR 03-JUL-1997; 97US-00887977.  
 PR 03-JAN-2002; 2002US-00039659.  
 XX (WANG/) WANG W.  
 PA (GISH/) GISH K C.  
 PA (SCHA/) SCHALL T J.  
 PA (VICA/) VICARI A.  
 PA (ZLOT/) ZLOTNIK A.  
 XX Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;  
 XX WPI; 2004-533376/51.  
 XX New substantially pure or isolated Thymus Expressed Chemokine (TECK),  
 PT useful for treating conditions associated with abnormal physiology or  
 PT development, including inflammatory conditions, e.g. asthma.  
 XX Disclosure; SEQ ID NO 14; 54pp; English.  
 XX The invention relates to a substantially pure or isolated polypeptide  
 CC comprises the mature protein of human TECK (thymus expressed chemokine)  
 CC whose full length sequence appears as ADQ67837. Also included are an  
 CC isolated or recombinant nucleic acid encoding mature TECK, an expression  
 CC vector comprising the nucleic acid, a host cell comprising the expression  
 CC vector and a method for producing the polypeptide. Also disclosed are the  
 CC mouse TECK cDNA and protein, human chemokines MIP-3alpha and MIP-3beta  
 CC (and their encoding cDNAs), and the cDNAs and encoded proteins  
 CC corresponding to human chemokine receptors DCCR (dendritic cell receptor  
 CC for chemokine) and M/DCCR (Monocyte/dendritic cell receptor for  
 CC chemokine). The polypeptide is useful for treating conditions associated  
 CC with abnormal physiology or development, including inflammatory  
 CC conditions, e.g. asthma. The present sequence represents a human

CC chemokine receptor showing sequence similarity to M/DCCR.

XX SQ Sequence 374 AA;  
Query Match 100.0%; Score 1970; DB 8; Length 374;  
Best Local Similarity 100.0%; Pred. No. 5.1e-215;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLSTSRSPFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60  
Db 1 MLSTSRSPFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60  
Qy 61 MLVLLILINCKKCLDIYLLINLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
Db 61 MLVLLILINCKKCLDIYLLINLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
Qy 121 HIGYFGGIFPFIILLTDRLYLAVHVPALKARTVTFGVTSVITLWLVAFASVPGIIFTK 180  
Db 121 HIGYFGGIFPFIILLTDRLYLAVHVPALKARTVTFGVTSVITLWLVAFASVPGIIFTK 180  
Qy 181 CQKEDSVVCGPYPPFRGNWPHITMNRILGLVPLLMVICYSGILKTLRLCRNEKKRHR 240  
Db 181 CQKEDSVVCGPYPPFRGNWPHITMNRILGLVPLLMVICYSGILKTLRLCRNEKKRHR 240  
Qy 241 AVRVIPTIMIVYFLFTWTPYINIVILLNTFQEPFGLSNCESTSQLDQATQVETLGMTHCCI 300  
Db 241 AVRVIPTIMIVYFLFTWTPYINIVILLNTFQEPFGLSNCESTSQLDQATQVETLGMTHCCI 300  
Qy 301 NPPIYAFVGEKFRSLFHIALGCRITAPLQKPVCGGVRPGKNVKTQTQGLLDGRGKSI 360  
Db 301 NPPIYAFVGEKFRSLFHIALGCRITAPLQKPVCGGVRPGKNVKTQTQGLLDGRGKSI 360  
Qy 361 GRAPEASLQDKEGA 374  
Db 361 GRAPEASLQDKEGA 374

RESULT 9  
ABG92881  
ID ABG92881 standard; peptide; 344 AA.  
AC ABG92881;  
XX 19-NOV-2002 (first entry)  
XX Class I receptors WSXWS motif.  
XX Immunoglobulin; variable heavy chain; variable light chain; human;  
KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;  
KW immunologic deficiency syndrome; blood protein disorder; nephritis;  
KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;  
KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;  
KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;  
KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;  
KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;  
KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;  
KW lymphocytopenia.  
XX Synthetic.  
OS  
XX WO200264612-A2.  
XX  
XX 22-AUG-2002.  
XX  
XX 08-FEB-2002; 2002WO-US003634.  
XX  
XX 09-FEB-2001; 2001US-00779880.  
XX 09-FEB-2001; 2001WO-US004153.  
XX 12-JUN-2001; 2001US-0297257P.  
XX 08-AUG-2001; 2001US-0310458P.  
XX 12-OCT-2001; 2001US-0328447P.  
XX 21-DEC-2001; 2001US-0341725P.  
XX

(HUMA-) HUMAN GENOME SCI INC.  
Roschke V, Rosen CA, Ruben SM;  
WPI; 2002-643455/69.  
New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.  
Example 17; Page 386; 562pp; English.  
The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of an amino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.18B5, XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody is useful treating, preventing, ameliorating, prognosing or monitoring cancers or other diseases or disorders e.g. immunologic deficiency syndromes such as blood protein disorders and ataxia telangiectasia, inflammation associated disorders such as endotoxin lethality, nephritis and inflammatory bowel disease, conditions associated with an increase in certain haematopoietic cells such as histiocytosis, defective or aberrant chemotaxis of immune cells or T-cell antigen presenting cell interaction, an infectious disease, an autoimmune disease such as Addison's disease, dermatitis and rheumatoid arthritis, allergies, a neurodegenerative disorder, a viral infection e.g. HIV infection, cytomegalovirus or poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma, cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a disease or disorder associated with aberrant expression of novel human G-protein chemokine receptor (CCRS) HDGNR10. This is the amino acid sequence of the WSXWS motif found in class I receptors

XX SQ Sequence 344 AA;  
Query Match 92.5%; Score 1823; DB 5; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2.5e-198;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 18 BEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGNMLVLLINCKKCLIT 77  
Db 1 BEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGNMLVLLINCKKCLIT 60  
Qy 78 DIVLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLVHIGYFGGIFPFIILLTID 137  
Db 61 DIVLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLVHIGYFGGIFPFIILLTID 120  
Qy 138 RYLAIHAVAFALKARTVTFGVTSVITLWLVAFASVPGIIFTKCKEDSVVVCYPPFRG 197  
Db 121 RYLAIHAVAFALKARTVTFGVTSVITLWLVAFASVPGIIFTKCKEDSVVVCYPPFRG 180  
Qy 198 WNNFHTMNRILGLVPLLMVICYSGILKTLRLCRNEKKRHRARVIFTIMIVYFLFTW 257  
Db 181 WNNFHTMNRILGLVPLLMVICYSGILKTLRLCRNEKKRHRARVIFTIMIVYFLFTW 240  
Qy 258 PYNIVILLNTFQEPFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLFH 317  
Db 241 PYNIVILLNTFQEPFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLFH 300  
Qy 318 IALGCRITAPLQKPVCGGVRPGKNVKTQTQGLLDGRGKSI 361  
Db 301 IALGCRITAPLQKPVCGGVRPGKNVKTQTQGLLDGRGKSI 344  
RESULT 10  
ABU61655  
ID ABU61655 standard; protein; 344 AA.  
XX ABU61655;  
XX  
DT 08-AUG-2003 (first entry)

XX DE Human monocyte chemoattractant protein 1 (MCP-1) receptor.  
 XX KW Human; G-protein chemokine receptor; receptor; HDGMR10; MCP-1;  
 XX 7-transmembrane receptor; monocyte chemoattractant protein 1.  
 XX OS Homo sapiens.  
 XX PN US2003023044-A1.  
 XX PD 30-JAN-2003.  
 XX PF 03-SEP-2002; 2002US-00232686.  
 XX PR 06-JUN-1995; 95US-00466343.  
 XX PR 18-NOV-1998; 98US-00195662.  
 XX PR 25-JUN-1999; 99US-00339912.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX PA Li Y, Ruben SM;  
 XX PI WPI; 2003-456307/43.  
 XX DR Producing an antibody, involves immunizing an animal with a polypeptide  
 XX PT or with a polypeptide encoded by the human G-protein chemokine receptor  
 XX PT clone in ATCC 97183, and recovering the antibody.  
 XX PS Disclosure; Fig 2; 23pp; English.  
 XX CC The invention relates to a method of producing an antibody, involving  
 CC immunising an animal with a human G-protein chemokine receptor (HDGMR10)  
 CC polypeptide (also referred to as a human 7-transmembrane receptor) and  
 CC recovering an antibody which binds the polypeptide. The method is useful  
 CC for producing an antibody which binds specifically to the human G-protein  
 CC chemokine receptor polypeptide. This sequence represents the monocyte  
 CC chemoattractant protein 1 (MCP-1) receptor which shares homology with the  
 CC HDGMR10 polypeptide of the invention  
 XX SQ Sequence 344 AA;  
 Query Match 92.5%; Score 1823; DB 6; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-198;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 18 EVVTFDDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGNMVLVLLINCKKLKCLT 77  
 DB 1 EVVTFDDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGNMVLVLLINCKKLKCLT 60  
 QY 78 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFPILLTID 137  
 DB 61 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFPILLTID 120  
 QY 138 RYLAIHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTRCKQEDSVVCGPYPPRG 197  
 DB 121 RYLAIHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTRCKQEDSVVCGPYPPRG 180  
 QY 198 WNNFHTIMRNILGLVPLLMVICYSGLKTLRCRNEKRRHRAVRVIFTIMIVYFLFWT 257  
 DB 181 WNNFHTIMRNILGLVPLLMVICYSGLKTLRCRNEKRRHRAVRVIFTIMIVYFLFWT 240  
 QY 258 PYNIVILLNTFQEPFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 317  
 DB 241 PYNIVILLNTFQEPFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 300  
 QY 318 IALGCRITAPLQKPVCGGVRPGNNRVKVTITQGLDGRGKSGIS 361  
 DB 301 IALGCRITAPLQKPVCGGVRPGNNRVKVTITQGLDGRGKSGIS 344  
 RESULT 11  
 ADF72129  
 ID ADF72129 standard; protein; 344 AA.

XX ADF72129;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Human G-protein chemokine receptor (CCR5) ligand MCP-1.  
 XX KW cytostatic; CCR5 modulator; antibody; G-protein chemokine receptor; CCR5;  
 KW cancer detection; cancer diagnosis; cancer prognosis; cancer monitoring;  
 KW cancer; hyperproliferative disorder; human; HDGMR10; ligand; MCP-1.  
 XX OS Homo sapiens.  
 XX PN US2003166024-A1.  
 XX PD 04-SEP-2003.  
 XX PF 01-MAY-2002; 2002US-00135839.  
 XX PR 09-FEB-2000; 2000US-0181258P.  
 XX PR 09-MAR-2000; 2000US-0187999P.  
 XX PR 22-SEP-2000; 2000US-0234336P.  
 XX PR 09-FEB-2001; 2001US-00779879.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX PA Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX PI WPI; 2003-898066/82.  
 XX DR New polypeptide comprising domains of an antibody that binds G-protein  
 XX PT chemokine receptor CCR5 is useful to detect, diagnose, prognose or  
 XX PT monitor cancers and other hyperproliferative disorders and to treat or  
 XX PT prevent a disease or disorder.  
 XX PS Disclosure; SEQ ID NO 9; 179pp; English.  
 XX CC The invention describes a new isolated polynucleotide that encodes an  
 CC antibody (AB1) comprising an amino acid sequence of at least one, two or  
 CC three complementarity determining regions (CDR) of a heavy chain variable  
 CC (VH) domain of an antibody (AB2) that immunospecifically binds to a G-  
 CC protein chemokine receptor (CCR5), at least one, two or three CDR regions  
 CC of a light chain variable (VL) domain of AB2 or at least one, two or  
 CC three CDR regions of both a VH and a VL domain of AB2. The antibody is  
 CC useful for detecting, diagnosing, prognosing or monitoring cancers and  
 CC other hyperproliferative disorders and for treating, preventing or  
 CC ameliorating a disease or disorder. This is the amino acid sequence of  
 CC MCP-1, a ligand of human G protein chemokine receptor (CCR5) HDGMR10.  
 XX SQ Sequence 344 AA;  
 Query Match 92.5%; Score 1823; DB 7; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-198;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 18 EVVTFDDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGNMVLVLLINCKKLKCLT 77  
 DB 1 EVVTFDDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGNMVLVLLINCKKLKCLT 60  
 QY 78 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFPILLTID 137  
 DB 61 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFPILLTID 120  
 QY 138 RYLAIHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTRCKQEDSVVCGPYPPRG 197  
 DB 121 RYLAIHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTRCKQEDSVVCGPYPPRG 180  
 QY 198 WNNFHTIMRNILGLVPLLMVICYSGLKTLRCRNEKRRHRAVRVIFTIMIVYFLFWT 257  
 DB 181 WNNFHTIMRNILGLVPLLMVICYSGLKTLRCRNEKRRHRAVRVIFTIMIVYFLFWT 240  
 QY 258 PYNIVILLNTFQEPFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 317  
 DB 241 PYNIVILLNTFQEPFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 300



Db 241 PYNIVILLNTQBFGLSNCESTSQLDOATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 300

Qy 318 IALGCRAPLQKPGVGGPGRGNKVVTTQGLDGRGKSGS 361  
 |||||  
 Db 301 IALGCRAPLQKPGVGGPGRGNKVVTTQGLDGRGKSGS 344  
 |||||

RESULT 12  
 ADP86217  
 ID ADP86217 standard; protein; 344 AA.  
 XX  
 AC ADP86217;  
 XX  
 DT 12-AUG-2004 (first entry)  
 DE Human MCP-1 receptor protein.  
 XX  
 KW G-protein chemokine receptor; HDGNR10; CCR5; haematopoiesis;  
 KW wound healing; coagulation; angiogenesis; tumour; chronic infection;  
 KW leukaemia; T-cell mediated autoimmune diseases; parasitic infection;  
 KW psoriasis; allergy; anaphylaxis; atherogenesis; malignancy; inflammation;  
 KW prostaglandin-independent fever; bone marrow failure; silicosis;  
 KW sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome;  
 KW human; MCP-1 receptor; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6743594-B1.  
 XX  
 PD 01-JUN-2004.  
 XX  
 PF 11-FEB-2000; 2000US-00502784.  
 XX  
 PR 06-JUN-1995; 95US-00466343.  
 PR 18-NOV-1998; 98US-00195662.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Li Y, Ruben SM;  
 XX  
 DR WPI; 2004-459648/43.  
 XX  
 PT Screening compounds binding to G-protein chemokine receptor HDGNR10,  
 PT involves contacting test compound with polypeptide of HDGNR10, and  
 PT observing binding of test compound to polypeptide.  
 XX  
 PS Disclosure; SEQ ID NO 9; 26pp; English.  
 XX  
 CC The invention relates to a method for screening compounds which bind the  
 CC G-protein chemokine receptor HDGNR10 (CCR5). Compounds identified by the  
 CC method of the invention are useful for stimulating haematopoiesis, wound  
 CC healing, coagulation, angiogenesis, for treating solid tumours, chronic  
 CC infections, leukaemia, T-cell mediated autoimmune diseases, parasitic  
 CC infections, psoriasis and for stimulating growth factor activity. The  
 CC compounds are also useful for treating allergy, anaphylaxis,  
 CC atherogenesis, malignancy, chronic and acute inflammation, histamine and  
 CC Ige-mediated allergic reactions, prostaglandin-independent fever, bone  
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and  
 CC hyper-eosinophilic syndrome. The present sequence is a human MCP-1  
 CC receptor protein. This sequence is used in the invention.  
 XX  
 SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 8; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-198;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ECVTFDDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFGFGVGNMLVLLINCKKLKCLT 77  
 |||||

Db 1 ECVTFDDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFGFGVGNMLVLLINCKKLKCLT 60  
 |||||

Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137  
 |||||

Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy 138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIITKCKEDSVVCGPYFPRG 197  
 |||||

Db 121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIITKCKEDSVVCGPYFPRG 180  
 |||||

Qy 198 WNFHTTMRNITLGLVPLLLIMVICYSGLIKTLTLRCRNEKKHRAVRVITIMIVVFLFWT 257  
 |||||

Db 181 WNFHTTMRNITLGLVPLLLIMVICYSGLIKTLTLRCRNEKKHRAVRVITIMIVVFLFWT 240  
 |||||

Qy 258 PYNIVILLNTQBFGLSNCESTSQLDOATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 317  
 |||||

Db 241 PYNIVILLNTQBFGLSNCESTSQLDOATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 300  
 |||||

Qy 318 IALGCRAPLQKPGVGGPGRGNKVVTTQGLDGRGKSGS 361  
 |||||

Db 301 IALGCRAPLQKPGVGGPGRGNKVVTTQGLDGRGKSGS 344  
 |||||

RESULT 13  
 AAB46859  
 ID AAB46859 standard; protein; 329 AA.  
 XX  
 AC AAB46859;  
 XX  
 DT 16-AUG-2001 (revised)  
 DT 02-AUG-2001 (revised)  
 DT 04-MAY-2001 (first entry)  
 XX  
 DE Human MCP-1 receptor protein fragment.  
 XX  
 KW HDGNR10; human; G-protein chemokine receptor; antiinflammatory;  
 KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;  
 KW cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;  
 KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;  
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;  
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;  
 KW anaphylaxis; malignancy; inflammation; histamine; Ige; silicosis; shock;  
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;  
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;  
 KW hyper-eosinophilic syndrome; vulneryary.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2001000241-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 29-NOV-2000; 2000US-00725285.  
 XX  
 PR 06-JUN-1995; 95US-00466343.  
 PR 18-NOV-1998; 98US-00195662.  
 PR 25-JUN-1999; 99US-00339912.  
 XX  
 PA (LIYY/) LI Y.  
 PA (RUBE/) RUBEN S M.  
 XX  
 PI Li Y, Ruben SM;  
 XX  
 DR WPI; 2001-226317/23.  
 XX  
 PT New human G-protein chemokine receptor polypeptides and polynucleotides,  
 PT useful for identifying (ant)agonists to the G-protein chemokine receptor.  
 XX  
 PS Disclosure; Page 16-17; 22pp; English.  
 XX  
 CC This invention describes a novel receptor polypeptide (I) selected from  
 CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the  
 CC specification; and (ii) a polypeptide encoded by the cDNA contained in a  
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The  
 CC products of the invention have antiinflammatory, immunomodulatory,  
 CC anticoagulant, antiallergic, immunosuppressive, vulneryary, cytostatic,  
 CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic

CC activity and can be used for gene therapy. The G-protein chemokine  
 CC receptors, HDGNR10, (1) are useful for screening for compounds which  
 CC activate or inhibit activation of (1). The products of the invention can  
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,  
 CC angiogenesis, treating solid tumours, chronic infections, leukaemia, T-  
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and  
 CC stimulating growth factor activity. HDGNR10 is useful for treating  
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic  
 CC reactions, prostaglandin-independent fever, bone marrow failure,  
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-  
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct  
 CC errors in the keyword formatting)  
 XX  
 SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 4; Length 329;  
 Best Local Similarity 95.6%; Pred. No. 1.8e-187;  
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;  
 QY 18 EVVTFDDYDYGAPCHKFDVKQIGAOQLPPLYSIVFIQFVGNMVLVLLINCKLKCLT 77  
 DB 1 EEVTFDDYDYGAPCHKFDVKQIGAOQLPPLYSIVFIQFVGNMVLVLLINCKLKCLT 60  
 QY 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFPILLITID 137  
 DB 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105  
 QY 138 RYLAIVHAVFALKARTVTGVTSTVITLWVAVPASVPGIIFTCKQKEDSVYVCGPYPPRG 197  
 DB 106 RYLAIVHAVFALKARTVTGVTSTVITLWVAVPASVPGIIFTCKQKEDSVYVCGPYPPRG 165  
 QY 198 WNNFHTIMRNILGLVPLLMVLCYSGLIKTLRCNEKRRHRAVRVIFTIMIVYFLFWT 257  
 DB 166 WNNFHTIMRNILGLVPLLMVLCYSGLIKTLRCNEKRRHRAVRVIFTIMIVYFLFWT 225  
 QY 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKRSLEH 317  
 DB 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKRSLEH 285  
 QY 318 IALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKSG 361  
 DB 286 IALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKSG 329

RESULT 14  
 ABB81055  
 ID ABB81055 standard; protein; 329 AA.  
 XX  
 AC ABB81055;  
 XX

DT 05-NOV-2002 (first entry)  
 XX

DE Human MCP-1 receptor.  
 XX

XX 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;  
 KW G-protein chemokine receptor; haematopoietic; immunosuppressant;  
 KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;  
 KW antirheumatic; antiarthritic; gene therapy; human; MCP-1; receptor.  
 XX

OS Homo sapiens.  
 XX

XX US2002076745-A1.  
 PN

XX 20-JUN-2002.  
 PD

XX 18-NOV-1998; 98US-00195662.  
 XX

PR 06-JUN-1995; 95US-00466343.  
 PR

XX (LIYY/) LI Y.  
 PA

PA (RUBE/) RUBEN S M.  
 XX

XX  
 XX

PI Li Y, Ruben SM;  
 XX WPI; 2002-598724/64.  
 DR  
 XX New polynucleotide encoding a human G protein chemokine receptor HDGNR10,  
 PT useful e.g. for treating tumors.  
 XX  
 PS Example; Fig 2; 22pp; English.  
 XX  
 CC The invention relates to a novel human 7-transmembrane receptor, HDGNR10,  
 CC which has been identified as a G-protein chemokine receptor. The GPCR  
 CC HDGNR10 polypeptide can be expressed by standard recombinant methodology.  
 CC Compounds that activate or inhibit the receptor polypeptide, optionally  
 CC expressed from DNA in gene therapy vectors, are used to treat diseases  
 CC that require: (a) activation of the receptor (e.g. stimulation of  
 CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune  
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the  
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis  
 CC etc). The present sequence represents a human MCP-1 receptor used in  
 CC comparison studies with the HDGNR10 receptor  
 XX  
 SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 5; Length 329;  
 Best Local Similarity 95.6%; Pred. No. 1.8e-187;  
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;  
 QY 18 EVVTFDDYDYGAPCHKFDVKQIGAOQLPPLYSIVFIQFVGNMVLVLLINCKLKCLT 77  
 DB 1 EEVTFDDYDYGAPCHKFDVKQIGAOQLPPLYSIVFIQFVGNMVLVLLINCKLKCLT 60  
 QY 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFPILLITID 137  
 DB 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105  
 QY 138 RYLAIVHAVFALKARTVTGVTSTVITLWVAVPASVPGIIFTCKQKEDSVYVCGPYPPRG 197  
 DB 106 RYLAIVHAVFALKARTVTGVTSTVITLWVAVPASVPGIIFTCKQKEDSVYVCGPYPPRG 165  
 QY 198 WNNFHTIMRNILGLVPLLMVLCYSGLIKTLRCNEKRRHRAVRVIFTIMIVYFLFWT 257  
 DB 166 WNNFHTIMRNILGLVPLLMVLCYSGLIKTLRCNEKRRHRAVRVIFTIMIVYFLFWT 225  
 QY 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKRSLEH 317  
 DB 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKRSLEH 285  
 QY 318 IALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKSG 361  
 DB 286 IALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKSG 329

RESULT 15  
 ADR16266  
 ID ADR16266 standard; protein; 329 AA.  
 XX

AC ADR16266;  
 XX

DT 21-OCT-2004 (first entry)  
 XX

DE Human MCP-1 receptor protein fragment.  
 XX

XX G-protein chemokine receptor; CCR5; HDGNR10; allergy; atherogenesis;  
 KW anaphylaxis; malignancy; inflammation; prostaglandin-independent fever;  
 KW bone marrow failure; silicosis; sarcoidosis; rheumatoid arthritis; shock;  
 KW hyper eosinophilic syndrome; haematopoiesis; wound healing; coagulation;  
 KW angiogenesis; solid tumour; chronic infection; leukaemia;  
 KW autoimmune disease; parasitic infection; psoriasis; human;  
 KW MCP-1 receptor; receptor.  
 XX

OS Homo sapiens.  
 XX

XX US2004151719-A1.  
 PN



THIS PAGE IS LEFT BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:29:43 ; Search time 25.9864 Seconds  
(without alignments)  
1384.767 Million cell updates/sec

Title: US-10-791-166-2  
Perfect score: 170  
Sequence: 1 MLSTSRFRFINTNESGEV.....GKGKSIGRAPEASIQDKEGA 374

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	374	2	138450 chemokine (C-C) re
2	1651.5	83.8	360	2	JC2443 chemokine (C-C) re
3	1224	62.1	352	2	A43113 chemokine (C-C) re
4	967.5	49.1	355	2	A45177 chemokine (C-C) re
5	960	48.7	359	2	I49341 MIP-1 alpha recept
6	902.5	45.8	355	2	I49339 macrophage inflam
7	890.5	45.2	355	2	G02436 chemokine (C-C) re
8	833	42.3	360	2	JC4587 chemokine (C-C) re
9	831.5	42.2	360	2	A57160 chemokine (C-C) re
10	794.5	40.3	383	2	S85594 G protein-coupled
11	731	37.1	356	2	I49340 MIP-1 alpha recept
12	723	36.7	355	2	JC5067 G protein-coupled
13	704.5	35.8	354	2	I58186 probable G protein
14	698	35.4	355	2	JC4304 orphan G protein-c
15	644.5	32.7	344	2	JC5942 chemokine receptor
16	584	29.6	378	2	B55735 lymphocyte-specifi
17	575.5	29.2	378	2	A55735 G protein-coupled
18	570	28.9	378	2	A45680 G protein-coupled
19	554.5	28.1	369	2	JC5068 G protein-coupled
20	541.5	27.5	360	2	A53611 interleukin-8 rece
21	537	27.3	359	2	A48921 interleukin-8 rece
22	531	27.0	352	2	G00048 fusin (LESTRA) - c
23	530.5	26.9	353	2	neuropeptide Y/pep
24	529.5	26.9	355	2	J28787 interleukin-8 rece
25	528	26.8	352	2	A45747 neuropeptide Y/pep
26	526	26.7	358	2	A53752 interleukin-8 rece
27	526	26.7	367	2	J50349 interferon-inducib
28	524.5	26.6	350	2	A39445 interleukin-8 rece
29	523	26.5	356	2	S42096 interleukin-8 rece

30	519	26.3	333	2	165989 G protein-coupled
31	484	24.6	350	2	JN0621 G protein-coupled
32	480	24.4	359	2	A42656 angiotensin II rec
33	479.5	24.3	374	2	S42628 G protein-coupled
34	475	24.1	359	2	I51372 angiotensin II rec
35	473	24.0	359	2	JC2134 angiotensin II rec
36	472	24.0	359	2	JH0621 angiotensin II rec
37	471	23.9	359	2	S15403 angiotensin II rec
38	471	23.9	359	2	JQ1516 angiotensin II rec
39	469	23.8	359	2	JC1104 angiotensin II rec
40	468	23.8	359	2	S44425 angiotensin II rec
41	465	23.6	359	2	JC1194 angiotensin II rec
42	465	23.6	374	2	S32785 G protein-coupled
43	464	23.6	359	2	A48857 angiotensin II rec
44	461.5	23.4	372	2	S26667 G protein-coupled
45	460.5	23.4	327	2	S56162 MDCR15 protein - h

ALIGNMENTS

RESULT 1

I38450  
Chemokine (C-C) receptor 2, splice form A - human  
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: I38450  
R:Charo, I.P.; Myers, S.J.; Heiman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant prot  
A:Reference number: A53477; MUID:94195821; PMID:8146186  
A:Accession: I38450  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <RES>  
A:Cross-references: UNIPROT:P41597; EMBL:U03882; NID:9472555; PIDN:AAA19119.1; PID:947255  
C:Genetics:  
A:Gene: GDB:CMKBR2  
A:Cross-references: GDB:337364; OMIM:601267  
A:Map position: 3p21-3p21  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane  
F:44-68/Domain: transmembrane #status predicted <TM1>  
F:79-99/Domain: transmembrane #status predicted <TM2>  
F:115-136/Domain: transmembrane #status predicted <TM3>  
F:154-178/Domain: transmembrane #status predicted <TM4>  
F:208-226/Domain: transmembrane #status predicted <TM5>  
F:244-265/Domain: transmembrane #status predicted <TM6>  
F:292-309/Domain: transmembrane #status predicted <TM7>  
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1970; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 1e-164;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRFRFINTNESGEVTFPDYDGAPCHKFDVKQIGALPLPLYSLVFIFFGVGN 60

Db 1 MLSTSRFRFINTNESGEVTFPDYDGAPCHKFDVKQIGALPLPLYSLVFIFFGVGN 60

Qy 61 MLVVLILINCKKLCITDIYLLNLAISDLFLITPLWAHSAANEVFGNACKLFTGLY 120

Db 61 MLVVLILINCKKLCITDIYLLNLAISDLFLITPLWAHSAANEVFGNACKLFTGLY 120

Qy 121 HIGYFGGIFPIILLITIDRYLAIVHAFALKARTVTFGVTSTVITLWAVFASVPGIIFTK 180

Db 121 HIGYFGGIFPIILLITIDRYLAIVHAFALKARTVTFGVTSTVITLWAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYPPRGNNFHTIMRNILGLVPLLIWVICYSIGILKTLRCRNEKKRHR 240

Db 181 CQKEDSVYVCGPYPPRGNNFHTIMRNILGLVPLLIWVICYSIGILKTLRCRNEKKRHR 240

```
Qy 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
Db 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300

Qy 301 NPIIYAVGKFRSLFHIALGCRIPALQKPVCGGPGVRPKQNVKVTQTQGLLDGRGKGS 360
Db 301 NPIIYAVGKFRSLFHIALGCRIPALQKPVCGGPGVRPKQNVKVTQTQGLLDGRGKGS 360

Qy 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

RESULT 2
JC2443
Chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine (C-C) receptor 5 - human
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
A;Reference number: JC2443; MUID:94324942; PMID:8048929
A;Accession: JC2443
A;Molecule type: mRNA
A;Residues: 1-360 <R>
A;Cross-references: UNIPROT:P41597; DBJ:J29984; NID:9531246; PIDN:BAA06253.1; PID:9531246
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of a human monocyte chemoattractant protein 1 receptor
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38463
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: 1-360 <RES>
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
F;43-70/Domain: transmembrane #status predicted <TM1>
F;81-100/Domain: transmembrane #status predicted <TM2>
F;115-126/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;207-226/Domain: transmembrane #status predicted <TM5>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;287-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Aen) (covalent) #status predicted
F;113-190/Disulfide bonds: #status predicted

Query Match 83.8%; Score 1651.5; DB 2; Length 360;
Best Local Similarity 95.5%; Pred. No. 7.1e-137;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRFRFTNTNESGEVTTTFDYDYGAPCHKFDVKQIQAQLLPPLYSLVIFGPGVN 60
Db 1 MLSTSRFRFTNTNESGEVTTTFDYDYGAPCHKFDVKQIQAQLLPPLYSLVIFGPGVN 60

Qy 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWHAASANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWHAASANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFPIILLTIDRYLAIAHVAFPALKARTVTFGVTTSVITLWVAVPASVPGIIFTK 180
Db 121 HIGYFGGIFPIILLTIDRYLAIAHVAFPALKARTVTFGVTTSVITLWVAVPASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPVPFGNNFHTIMRNILGLVPLLTIMVLCYSGLIKTLRCNEKKRRH 240
Db 181 CQKEDSVYVCGPVPFGNNFHTIMRNILGLVPLLTIMVLCYSGLIKTLRCNEKKRRH 240
```

```
Qy 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
Db 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300

Qy 301 NPIIYAVGKFR---SLP---HIALG-CRIAPL 327
Db 301 NPIIYAVGKFRYLVSFFPRKHITKRFCKQCPV 334

RESULT 3
A43113
Chemokine (C-C) receptor 5 - human
N;Alternate names: C-C CKR-5; CCR5
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C;Accession: A43113; S71808; A58834; A58832; G02653; A58833
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
A;Reference number: A43113; MUID:96241590; PMID:8639485
A;Accession: A43113
A;Molecule type: mRNA
A;Residues: 1-352 <SAM1>
A;Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti, M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.
Nature 382, 722-725, 1996
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the CCR-5 chemokine receptor gene
A;Reference number: S71808; MUID:96345670; PMID:8751444
A;Accession: S71808
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 182-206;207-230 <SAM2>
A;Accession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-184,'INDSLGAGPAAACHGHLGNPKNSASVSK' <SAM3>
A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A;Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor
A;Reference number: A58832; MUID:96295970; PMID:8699119
A;Accession: A58832
A;Molecule type: mRNA
A;Residues: 1-352 <COM1>
A;Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R;Combadiere, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01541
A;Accession: G02653
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-89,'L',91-352 <COM2>
A;Cross-references: EMBL:U57840
R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor
A;Reference number: A58833; MUID:96291862; PMID:8663314
A;Accession: A58833
A;Molecule type: mRNA
A;Residues: 1-352 <RAP>
A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30574), and dual-tropic strains of HIV-1 bind to a complex of chemokine receptors
C;Genetics:
A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
A;Function:
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
```

A;Note: probably acts to control granulocyte proliferation and differentiation  
C;Superfamily: vertebrate rhodopsin  
F;32-56/Domain: transmembrane #status predicted <TM1>  
F;67-87/Domain: transmembrane #status predicted <TM2>  
F;103-124/Domain: transmembrane #status predicted <TM3>  
F;142-166/Domain: transmembrane #status predicted <TM4>  
F;193-218/Domain: transmembrane #status predicted <TM5>  
F;236-257/Domain: transmembrane #status predicted <TM6>  
F;285-300/Domain: transmembrane #status predicted <TM7>  
F;20-269,101-178/disulfide bonds: #status predicted  
F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted  
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 62.1%; Score 1224; DB 2; Length 352;  
Best Local Similarity 76.3%; Pred. No. 1.8e-99;  
Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;

Qy 24 PDYD--GAPCHKFDVKGQIAGQLLPPLYSVIFGFGVGNMVLVLINCKLCLTDIYL 81  
Db 10 YDINYTSEPCQKINVKQIARLLPPLYSVIFGFGVGNMVLVLINCKLKSMTDIYL 69

Qy 82 LNLALSLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYGGIFFIILLTIDRYLA 141  
Db 70 LNLALSLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYGGIFFIILLTIDRYLA 129

Qy 142 IVHAFVFAKARTVTFGVVTSVITWLVAFVAVPGIIFTKCKEDSVVCGYFPF---RG 197  
Db 130 VVHAFVFAKARTVTFGVVTSVITWLVAFVAVPGIIFTRSQEGLHTCSHFYPSQVQF 189

Qy 198 WNNPHTIMRNILGLVPLLMVICYSGLIKTLRCNEKKHRAVRVIFTIMIYVFLFWT 257  
Db 190 WKNFOTELKIVTLGLVPLLMVICYSGLIKTLRCNEKKHRAVRVIFTIMIYVFLFWA 249

Qy 258 PYNIVILLNTFOEFGLSNCESTSQLDOATVTTGLMTHCCINPIIYAFVGEKFRSLF- 316  
Db 250 PYNIVILLNTFOEFGLSNCESTSQLDOATVTTGLMTHCCINPIIYAFVGEKFRNYLL 309

Qy 317 -----HLA 319  
Db 310 VFFQKHIA 317

RESULT 4  
A45177  
chemokine (C-C) receptor 1 - human  
N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: A45177; I55671  
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.  
Cell 72, 415-425, 1993  
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-  
A;Reference number: A45177; MUID:93161416; PMID:7679328  
A;Accession: A45177  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-355 <NEO>  
A;Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417  
A;Experimental source: HL60 cells  
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)  
R;Gao, J.  
J. Exp. Med. 177, 1421-1427, 1993  
A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha  
A;Reference number: I55671; MUID:93240122; PMID:7683036  
A;Accession: I55671  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-355 <RES>  
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417  
C;Genetics:  
A;Gene: GDB:CMKBRI; CMKR-1

A;Cross-references: GDB:138446; OMIM:601159  
A;Map position: 3p21-3p21  
C;Superfamily: vertebrate rhodopsin  
F;36-60/Domain: transmembrane #status predicted <TM1>  
F;71-91/Domain: transmembrane #status predicted <TM2>  
F;108-129/Domain: transmembrane #status predicted <TM3>  
F;147-171/Domain: transmembrane #status predicted <TM4>  
F;205-223/Domain: transmembrane #status predicted <TM5>  
F;240-264/Domain: transmembrane #status predicted <TM6>  
F;288-305/Domain: transmembrane #status predicted <TM7>  
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;24-273,106-183/disulfide bonds: #status predicted  
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 49.1%; Score 967.5; DB 2; Length 355;  
Best Local Similarity 58.7%; Pred. No. 4.9e-77;  
Matches 185; Conservative 47; Mismatches 72; Indels 11; Gaps 5;

Qy 12 NTNESGEVTFPDYDYGAPCHKFDVKGQIAGQLLPPLYSVIFGFGVGNMVLVLINCK 71  
Db 5 NTTED-YDTTFPDYGDATPCQKVNRAFGAQLLPPLYSVIFGFGVGNMVLVLVQYK 63

Qy 72 KLKCLTDIYLINLAISDLLFLITLPLWA-HSAANEWFGNAMCKLFTGLYHIGYGGIFF 130  
Db 64 RLKNMTSIYLLNLAISDLLFLITLPLWIDYKLKDDWVFGDAMCKILSGFYVYTGYSIEFF 123

Qy 131 IILLTIDRYLAIVHAFVFAKARTVTFGVVTSVITWLVAFVAVPGIIFTKCKEDSVVVC 190  
Db 124 IILLTIDRYLAIVHAFVFAKARTVTFGVVTSIILWALAIALSMGLYFSKTQWFTHTC 183

Qy 191 GPVFP-----RGWNNPHTIMRNILGLVPLLMVICYSGLIKTLRCNEKKHRAVRVIF 246  
Db 184 SLHPHESLREWKLFQALKLNLGLVPLLMVICYGIILKILLRRPNEKK-SKAVRLIF 242

Qy 247 TIMVYFLPFTPNVIVILLNTFOEFGLSNCESTSQLDOATVTTGLMTHCCINPIIYA 306  
Db 243 VIMIFLFTPNVNLITLISVFQDFLFTHEQSRHLDLAVQVTEVIATYTHCCVNPVIYA 302

Qy 307 FVGEKF---RSLFH 317  
Db 303 FVGERFRKYLQFLH 317

RESULT 5  
I49341  
MIP-1 alpha receptor like-2 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I49341  
R;Gao, J.L.; Murphy, P.M.  
J. Biol. Chem. 270, 17494-17501, 1995  
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokir  
A;Reference number: I49339; MUID:95340546; PMID:7542241  
A;Accession: I49341  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-359 <RES>  
A;Cross-references: UNIPROT:Q8KM7; EMBL:U28406; NID:g881551; PID:g881552  
C;Superfamily: vertebrate rhodopsin

Query Match 48.7%; Score 960; DB 2; Length 359;  
Best Local Similarity 50.1%; Pred. No. 2.2e-76;  
Matches 187; Conservative 59; Mismatches 89; Indels 38; Gaps 7;

Qy 10 IRNTNESGEVTFPDYDYGAPCHKFDVKGQIAGQLLPPLYSVIFGFGVGNMVLVLIN 69  
Db 8 IKTVESFE--TTPYEYEWAPPCEKVKRIKELGSLWLLPPLYSVIFIGLLGNMVMVLILIK 65

Qy 70 CKKLKCLTDIYLINLAISDLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYGGI 128  
Db 66 YRKLQIMTNYLNLNLAISDLLFLITLPLWVHYNWFGHGMCKMLSGFYLYALYSEI 125

```
Qy 129 FFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITLWAVFASVPGIIFTCKQKEDSVY 188
Db 126 FFIILLIDRYLAIVHAVFALRARTVTFATITSITWGLAGLAALPFIHESQDSGEF 195
Qy 189 VCGPYFPRG----WNNFHTMRNLTGLVPLLMVICYSGILTKTLRCRNEKRRHRAVRV 244
Db 186 SCSPRYEGEBEDSWKRFALRMNIFGLALPLLVNVICYSIGIKTLRCPN-KKKHKAIRL 244
Qy 245 IFTIMIVFLFWPYNIVILNTFOEPFGLSNCSTSQLDOATQVTTGLMTHCCINPIL 304
Db 245 IFVVMIVFFIFWTFYNVLVLLFSFHSFTLESCQSKHLDLQVTEVIAVTHCCVNPVI 304
Qy 305 YAFVGEKFRS----LFIHALGCRAPLQKVPVCGPGVRPGKVKVTTQGL---LDGRGKG 357
Db 305 YAFVGERFRKHLRFFH-----RNQFTWENIFQFLPGENG 341
Qy 358 KSTGRAPESLQD 370
Db 342 RTSVSPSTGEQE 354

RESULT 6
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49339
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49339
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: UNIPROT:P51675; EMBL:U28404; NID:9881547; PIDN:AAA89153.1; PID:98815
C:Superfamily: vertebrate rhodopsin

Query Match 45.8%; Score 902.5; DB 2; Length 355;
Best Local Similarity 53.1%; Pred. No. 2.4e-71;
Matches 170; Conservative 58; Mismatches 75; Indels 17; Gaps 6;

Qy 21 TTFEDYDYGAPCHKFDVKQIGALLPPLYSILVTFIFGVGNMLVVLILINCKKLCLTDIY 80
Db 13 TTFEDYDSTFCQKTAFAAGALLPPLYSILVTFIFGVGNMLVVLILINCKKLCLTDIY 72
Qy 81 LLNLAISDLLFLITPLWA-HSANEVWFGNCKLFTGLYHIGYFGIGIFILLITDIDY 139
Db 73 LFNLAISDLLVFLFTPLWIDYKLDWIFGDAMCKLLSGFYLLGLYSEIIFILLITDIDY 132
Qy 140 LAIVHAVFALKARTVTFGVVTSVITLWAVFASVPGIIFTCKQKEDSVYVCGPYFPR- 195
Db 133 LAIVHAVFALRARTVTFGIITSITWALAILASMPALYFFPAQWFFHTRCSHPFPYKSL 192
Qy 196 RGWNNFHTMRNLTGLVPLLMVICYSGILTKTLRCRNEKRRHRAVRVFTIMIVVFLF 255
Db 193 KQWKRFOALKNLGLILPLLMVICYAGIIRLLR-RPEKKVKAVALFATLFLFLL 251
Qy 256 WTPYNIVILNTFOEPFGLSNCSTSQLDOATQVTTGLMTHCCINPILYAFVGEKF- 312
Db 252 WTPYNLSVFSVAFQDVLFTNQCEQSKHLDLQVTEVIAVTHCCVNPILYVFGVERFWKY 311
Qy 313 -RSLF--HIALGCRAPLQK 329
Db 312 LRQLFORHVAI-----FLAK 326

RESULT 7
G02436
chemokine (C-C) receptor 3 - human
N:Alternate names: C-C CKR-3
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
```

```
C:Accession: G02436; A57237
R:Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A:Reference number: H01272
A:Accession: G02436
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <PON>
A:Cross-references: UNIPROT:P51677; EMBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477
R:Combadire, C.; Anuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A:Reference number: A57237; MUID:95348056; PMID:7622448
A:Accession: A57237
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
A:Cross-references: GB:U28694; NID:gl199579; PIDN:AAC50469.1; PID:gl199580
A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1
C:Genetics:
A:Gene: GDB:CMKBR3
A:Cross-references: GDB:579624; OMIM:601268
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-261/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:24-273, 106-183/Disulfide bonds: #status predicted
F:245/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 45.2%; Score 890.5; DB 2; Length 355;
Best Local Similarity 54.6%; Pred. No. 2.7e-70;
Matches 167; Conservative 56; Mismatches 72; Indels 11; Gaps 5;

Qy 21 TTFEDYDYGAPCHKFDVKQIGALLPPLYSILVTFIFGVGNMLVVLILINCKKLCLTDIY 80
Db 14 TSYD-DVGLLCEKADTRALMAQFVPLPPLYSILVTFVGLLGNVVMILIKYRRURIMTNIY 72
Qy 81 LLNLAISDLLFLITPLWAHSA-ANENVWFGNCKLFTGLYHIGYFGIGIFILLITDIDY 139
Db 73 LLNLAISDLLFLVLPFWHYVGRHNWVFGHCKLLSGFYHTGLYSEIIFILLITDIDY 132
Qy 140 LAIVHAVFALKARTVTFGVVTSVITLWAVFASVPGIIFTCKQKEDSVYVCGPYFPR- 196
Db 133 LAIVHAVFALRARTVTFGVITSITWGLAVLAALPEFIFVETBELFEETLCSALYPEDTV 192
Qy 197 -GWNNFHTMRNLTGLVPLLMVICYSGILTKTLRCRNEKRRHRAVRVFTIMIVVFLF 255
Db 193 YSRHRFTLMTFICVLPLLVMAICYTGIIKTLRCPS-KKKYKAIRLIFVIMAVFIF 251
Qy 256 WTPYNIVILNTFOEPFGLSNCSTSQLDOATQVTTGLMTHCCINPILYAFVGEKFRS- 314
Db 252 WTPYNVAILSSYSQISILFGNDCERTKHLDLVLMVTEVIAVSHCCMPVIAVFGVERPKY 311
Qy 315 ---LFH 317
Db 312 LRHFFH 317

RESULT 8
JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: JC4587
R:Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
```



A:Reference number: JC4587; MUID:96136324; PMID:8573157  
A:Accession: JC4587  
A:Molecule type: mRNA  
A:Residues: 1-360 <HID>  
A:Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167851  
A:Experimental source: thymus  
C:Genetics:  
A:Gene: cc ckr-4  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus  
P:2,183/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:72,202,350/Binding site: phosphate (Ser) (covalent) by casein kinase II #status predicted  
P:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.3%; Score 833; DB 2; Length 360;  
Best Local Similarity 47.9%; Pred.No.2.9e-65;  
Matches 160; Conservative 63; Mismatches 89; Indels 22; Gaps 5;

QY 10 IRNTNSGEVTTFFDYD-YGACHFPDVKQIGAOQLLPPLYSLVFIPIFGVGNNMLVVLIIL 68  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 6 VTDITQDETYNYSYFYESMPKECTKEGIFKAQEVFLPPLYSVLVFLGLFGSNVVVLVF 65  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
QY 69 NCKKLCLTDLIYLNLAIISDLLFTLTPLWAHAANNEWFGNAMCKLFTGLYHIHYFGGI 128  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 66 KYRRLKSMTDVLYLNLAISDLLFVLSPFFGYGYAAQDWFGGLGCLKIVSNMVLGVFSYG 125  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
QY 129 FFIIILTIDRYLAIVHAVFALKARTVTFGVTVSWITWLVAVFASVPGIIFTKCQKEDSVY 188  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 126 FFMIMSIDRYLAIVHAVPSLKARTITYGVTSLLIWSAVAFSLPGLLFSTCYTEHNHT 185  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
QY 189 VCGPYF---PRGNWNFHTIMRNLTGLVLPILLIMIYCYSGLIKTLRCRNEKKRHRAVRVI 245  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 186 YCKTQYSVNSTTWKVLSSLEINVLLGLLPLGLIMLFWYSMIIRTLOHCKNEKK-NRAVRMI 244  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
QY 246 FTTIMVYVFLFWTPYINIVILLINTQRFEGLSNCSESTSOLDQATQVTFELGTHCCINPIIY 305  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 245 FGVVVLFLGFWTPYNVVFLFETLVELEVLDQCCTERYLDYAIQATETLGFIIHCCLNFVIY 304  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
QY 306 AFVGEKFR---SLFHIALGCRIAPLQKPVCGGP 335  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 305 FFLGKRPKYITQLFR-----TCRGP 325  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 9  
A57160  
Chemokine (C-C) receptor 4 - human  
N:Alternate names: C-C CKR-4  
C:Species: Homo sapiens (man)  
C:Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: A57160  
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W.  
J. Biol. Chem. 270, 19495-19500, 1995  
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor cd  
A:Reference number: A57160; MUID:95370289; PMID:7642634  
A:Accession: A57160  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-360 <POW>  
A:A/Cross-references: UNIPROT:P51679; GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g97145  
A>Note: source clone KS-5  
C:Genetics:  
A:Gene: GDB:CMKB84  
A:C/Superfamily: vertebrate rhodopsin  
C:Map position: 3p21-3p21  
P:76-97/Domain: transmembrane #status predicted <TM2>  
F:112-133/Domain: transmembrane #status predicted <TM3>  
F:151-175/Domain: transmembrane #status predicted <TM4>  
F:208-226/Domain: transmembrane #status predicted <TM5>  
F:243-264/Domain: transmembrane #status predicted <TM6>

[illegible]

[illegible]

RESULT 11  
I49340  
MIP-1 alpha receptor like-1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49340  
R:Gao, J.L.; Murphy, P.M.  
J. Biol. Chem. 270, 17494-17501, 1995  
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine  
A:Reference number: I49339; MUID:95340546; PMID:7542241  
A:Accession: I49340  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-356 <RES>  
A:Cross-references: UNIPROT:P51676; EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881549  
C:Superfamily: vertebrate rhodopsin

Query Match	37.1%;	Score 731;	DB 2;	Length 356;
Best Local Similarity	46.6%;	Pred. No. 2.4e-56;		
Matches 137;	Conservative 59;	Mismatches 92;	Indels 6;	Gaps 3;
QY	25	DYDYGAPCHFDYKQIGCAQALLPPLYSLSVFFEGFVGNMLVLLILNCKKLKCLTIDYLLNL	84	
DB	18	DFMSGGFCFSINVRAGFITPTPLYSLSVFIIGVIGHVLVVLVLOHKLRLNMTSYILFNL	77	
QY	85	AISDLLPLIITLPLWA-HSAANEWVFGNAMCKFLGLVHIGYFGGIFFIILLITIDRYLAIV	143	
DB	78	AISDLVFLSTLPLFWVDYIMKGDMIFGNAMCKFVSGFYGLYSDMFFITLLTIDRYLAIV	137	
QY	144	HAYFALKARTVTFCGVTSVITLWVAFPASVFGIIFTRCKQEDSVYVCGPYPPR----	199	
DB	138	HVVFALRARTVTGIISSIIITWLAALVSPCLAVFKSQMEFTVHTCRAILPKRSLIRFL	197	
QY	200	NFHTTMINIQLVLPLIMVICYSGILKTLRLCRNEKKRHRAVAVITFIMIVYFLFWTPY	259	
DB	198	RFQALTNWILGLIPLLAIIICYTRIINVLR-RPNKKCAVMRLIFVITLLFLLAPY	256	
QY	260	NIVILLNTPOBFGLSNCESTSQLDQATQVTTGTMTHCCINPLIYAFVGEKFR	313	
DB	257	YLAAFVSAFEDVLPTPSLRQOVDLSIMITEALAYTHCCVNPVIVYFVGVKRR	310	

RESULT 12  
JC5067  
G protein-coupled receptor CKR-L1 - human  
N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6  
C;Species: Homo sapiens (man)  
C;Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #text\_change 09-Jul-2004  
C;Accession: JC5067; G02776; G02387  
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.  
Biochem. Biophys. Res. Commun. 227, 846-853, 1996  
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like g  
A;Reference number: JC5067; MUID:97040707; PMID:8886020  
A;Accession: JC5067  
A;Molecule type: DNA  
A;Residues: 1-355 <ZAB>  
A;Cross-references: UNIPROT:P51685; EMBL:Z79782; NID:g1668735; PIDN:CAB02142.1; PID:g166  
R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.  
Submitted to the EMBL Data Library, June 1996  
A;Reference number: H01714  
A;Accession: G02776  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA

A;Residues: 1-355 <NAP>  
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979  
R;Bonner, T.I.  
submitted to the EMBL Data Library, January 1996  
A;Reference number: H01154  
A;Accession: G02387  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-355 <BON>  
A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057  
C;Comment: This protein belongs to the family of beta chemokine receptors  
C;Genetics:

C; Gene: GDB:CMKBR8; CMKBR12; TER1; CCR-11  
 A; Cross-references: GDB:6053733; OMIM:601834  
 A; Map position: 3p21-3p21  
 C; Superfamily: vertebrate rhodopsin  
 C; Keywords: G protein-coupled receptor; transmembrane protein  
 F; 36-63/Domain: transmembrane #status predicted <TM1>  
 F; 73-94/Domain: transmembrane #status predicted <TM2>  
 F; 108-129/Domain: transmembrane #status predicted <TM3>  
 F; 147-171/Domain: transmembrane #status predicted <TM4>  
 F; 200-222/Domain: transmembrane #status predicted <TM5>  
 F; 239-260/Domain: transmembrane #status predicted <TM6>  
 F; 281-304/Domain: transmembrane #status predicted <TM7>

Query Match	36.7%	Score	723;	DB 2;	Length	355;			
Best Local Similarity	43.5%;	Pred. No.	1.2e-55;						
Matches	131;	Conservative	59;	Mismatches	103;	Indels	8;	Gaps	3;
Qy	20	VTTFDFDYD	---	GAPCHKFDVQIGAGLLPPLYSIVFIQFVGNMLVLINCKKLLKC	75				
Db	9	VTVTDTYYDPDIFSSPCDABLIQNGKLLAAVFCLLFVFSLIGNSLIVLIVVCKKLR	68						
Qy	76	LTDIYLNLNLAISDLLFLITLPLWAHSAANWFVGNAMCKLFTGLYHIGYFGGIFFIILLT	135						
Db	69	ITDVLNLNLALSDLLFVFSFPFQTYLLDQWVEGTVMCKVSGFYIIGFYSSMFFITLMS	128						
Qy	136	IDRYLAIIVHAFALKARTVTFGVQVTSVITWLIVAFASVPGIITPKCKEKSUVVYCGFYFP	195						
Db	129	VDRYLAVVHAYALKVRTIRMGTTCLCAVWLTAIMATIPLLVFYQVASEDGVLCQCSFYN	188						
Qy	196	R--GWNNEFTIMRNILGLVLPILLIMVICSGLIKTLRCKNEKRHRVVRVFTIMIVY	252						
Db	189	QQTILWKIFNFKNNILGLLIPFTIFMFCYKILHLQKRCQNHKT-KAELVLIVVIAS	247						
Qy	253	FLFETPNYIVILLNTOEFFGLSNCESSTQDQATQVTTGLMTHCCINPIIYAFVGEKF	312						
Db	248	LLFWVPNVVLFTLSLHSMILDCSSISQQLTYATHVTEIISFTTHCCVNPVIYAFVGEKF	307						
Qy	313	R 313							
Db	308	K 308							

RESULT 13

I58186

probable G protein-coupled receptor - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: I58186

Harrison, J.K.; Barber, C.M.; Lynch, K.R.  
Neurosci. Lett. 169, 85-89, 1994

A/Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spin  
A/Reference number: I58186; MUID:94323113; PMID:8047298

A/Accession: I58186

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-354 <RES>

A/Cross-references: UNIPROT:P35411; EMBL:U04808; NID:Q2558635; PIDN:AA887099

A/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor

Query Match 35.8%; Score 704.5; DB 2; Length 354;

```

126 DRYLAIVLAANSNNRTVQHGVTISLGWAAAILVAAPQPMFTK-QKENE---CLGDYPE 181
197 GWNPHFTIMRNI-----LGLVPLLLIMVICYSGLIKTLRCRNEKGRHRAVRVIFTMIVY 252
182 VLQEIWPNLRNVTNFTGLFLPLLLINSYCFRIIQTLSFCKNHKKA-KAIKLLLVVIVF 240
253 FLEWTPYNIVILLNTQBFPGLSNCSESTSQLODAQTQVTEFLGTHHCCINPIIYAFVGEKF 312
241 FLEWTPYNVIMPLETKLYDFFPSCDMRKDLRLASVTETVAFSHCCINPLIYAFAGEKF 300
313 RS-LPHIALGCRAPLQKPVCG 333
301 RRYLYHLYGKCLAV-----LCG 317

RESULT 15
JC5942
chemokine receptor - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: JC5942
R:Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A:Title: Cloning and characterization of a novel human chemokine receptor.
A:Reference number: JC5942; MUID:98139902; PMID:9473515
A:Status: preliminary
A:Accession: JC5942
A:Molecule type: DNA
A:Residues: 1-344 <FAN>
A:Cross-references: UNIPROT:O00421; GB:U97123; NID:g2897070; PIDN:RAC39595.1; P
C:Superfamily: vertebrate rhodopsin

Query Match 32.7%; Score 644.5; DB 2; Length 344;
Best Local Similarity 39.9%; Pred. No. 8.7e-49;
Matches 132; Conservative 58; Mismatches 120; Indels 21; Gaps 6;

QY 27 DYGAPCHKEDVKIGIAQLPPLYSLVPIFGVGNMLVVLILINCKKCLKLTLDYLLMLAI 86
Db 23 DEAEQCDKYDAQALSQALVPSLCSAVFVIGVLDNLLVLLVLYKGLKRVENIYLLNLAV 82
QY 87 SDLLFLTLPLWAHSAANEVFGNANCKLFTGLYHIGYFGGIPFIILLTTIDRYLAIVH-A 145
Db 83 SNICFLLTLTPFWAHAG-----GDPWCKILIGLYFVGLYSETFNCNLTQVRYLVFLHKG 136
QY 146 VFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTKCKQSDSVYVCG----PYFPRG---W 198
Db 137 NFPSARRRVPCCIITSVLAWVTAILATLEPVYVYKQMEDQYKCAFSRTPELPADSETFW 196
QY 199 NNPHFTIMRNLGLVPLLLIMVICYSGLIKTLRCRNEKGRHRAVRVIFTMIVYFLEWTP 258
Db 197 KHPLETKMNIISVLVPLFIPTFLYVQMRKTL---RFRQRYSLFKLVFAIMVYVLLMWAP 253
QY 259 YNIVILLNTQBFPGLSNCSESTSQLODAQTQVTEFLGTHHCCINPIIYAFVGEKFS----- 314
Db 254 YNIAFFLSFTKEHFSUSDCKSSYNLDKSVHITKLIATHTCCINPLLYAFLDGTFSKYLCL 313
QY 315 LPHIALGCRAPLQKPVCGPGVGRPGKNVKV 345
Db 314 CFHLRNTPLQPGQAQGSREPDHSTEV 344

Search completed: June 9, 2005, 16:49:02
Job time : 26.9864 secs

```

Search completed: June 9, 2005, 16:49:02  
Job time : 26.9864 secs

**THIS PAGE LEFT BLANK  
BEST AVAILABLE COPY**

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

**THIS PAGE LEFT BLANK**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:28:38 ; Search time 115.665 Seconds  
(without alignments)  
1655.798 Million cell updates/sec

Title: US-10-791-166-2

Perfect score: 1970

Sequence: 1 MLSTSRFRFRNTNNSGEEV.....GKGSGIGRAPEASLDQKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1970	100.0	374	1 CCR2 HUMAN	P41597 homo sapien
2	1614.5	82.0	360	1 CCR2 MACMU	O18793 macaca mula
3	1346.5	68.4	373	1 CCR2 RAT	O55193 rattus norv
4	1332.5	67.6	373	1 CCR2 MOUSE	P51683 mus musculu
5	1327.5	67.4	373	1 CCR2 MOUSE	O5Yt42 sus scrofa
6	1252	63.6	352	2 Q95NC2	Q95nc2 callicebus
7	1247	63.3	354	2 Q68G28	Q68g28 rattus norv
8	1244	63.1	339	2 Q9TQ73	Q9tqt3 callithrix
9	1244	63.1	339	2 Q9TUV8	Q9tuv8 aguinus sp
10	1244	63.1	352	2 Q6WN98	Q6wn98 callithrix
11	1244	63.1	352	2 Q9M2A0	Q9mza0 callithrix
12	1243	63.1	354	1 CCR5 MOUSE	P51682 mus musculu
13	1243	63.1	339	2 Q9TQV5	Q9tqv5 aguinus sp
14	1243	63.1	352	2 Q95NC4	Q95nc4 ateles geof
15	1241	63.0	352	2 Q6WN93	Q6wn93 leontopithe
16	1241	63.0	352	2 Q6WN96	Q6wn96 leontopithe
17	1241	63.0	352	2 Q6WN97	Q6wn97 cebuella py
18	1240	62.9	339	2 Q9TUV0	Q9tuv0 aguinus sp
19	1239	62.9	352	2 Q6Yt41	Q6yt41 sus scrofa
20	1239	62.9	352	2 Q9MZ99	Q9mz99 ateles sp.
21	1238.5	62.9	339	2 Q9TUV6	Q9tuv6 aguinus sp
22	1238	62.8	339	2 Q9TUV1	Q9tuv1 aguinus sp
23	1237	62.8	339	2 Q9TUV9	Q9tuv9 aguinus sp
24	1236	62.7	339	2 Q9TQW0	Q9tqw0 hylobates c
25	1236	62.7	352	1 CCR5_CERTO	O62743 cercocebus
26	1236	62.7	352	1 CCR5_HYLLE	O97883 hylobates l
27	1236	62.7	352	2 Q8HZT9	Q8hzt9 saimiri sci
28	1236	62.7	352	2 Q6WN92	Q6wn92 leontopithe
29	1236	62.7	352	2 Q6WN94	O6wn94 leontopithe
30	1236	62.7	352	2 Q71R52	Q71rs2 cercocebus
31	1235	62.7	339	2 Q9T5N3	Q9tsn3 macaca fasc

32	1235	62.7	352	2	O77776	077776 cercocebus
33	1234	62.6	339	2	Q9TUV5	Q9tuv5 aguinus sp
34	1234	62.6	352	2	O6WN95	O6wn95 leontopithe
35	1233	62.6	339	2	Q9TUV2	Q9tuv2 alouatta ca
36	1233	62.6	352	2	O95NE1	O95ne1 cercocebus
37	1232	62.5	339	2	Q9TUT9	Q9tut9 macaca mula
38	1232	62.5	339	2	Q9TUV0	Q9tuv0 aotus trivi
39	1232	62.5	339	2	Q9TUV4	Q9tuv4 callithrix
40	1232	62.5	339	2	O9TUX0	Q9tux0 hylobates c
41	1232	62.5	352	2	O6WN91	O6wn91 brachyteles
42	1231	62.5	339	2	Q9TUV9	Q9tuv9 hylobates m
43	1231	62.5	352	1	CCR5_HYLM	O95nc0 hylobates c
44	1231	62.5	352	2	Q95NC9	Q95nc9 alouatta se
45	1231	62.5	352	2	Q9XT12	Q9xt12 cercopithec

## ALIGNMENTS

RESULT 1  
ID CCR2 HUMAN STANDARD; PRT; 374 AA.  
AC P41597;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE C-C chemokine receptor type 2 (C-C CCR-2) (CCR-2) (CCR2)  
GN (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).  
GN Name=CCR2; Synonyms=CMKBR2;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94195821; PubMed=8146186;  
RX Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,  
RA Coughlin S.R.;  
RT "Molecular cloning and functional expression of two monocyte  
chemoattractant protein 1 receptors reveals alternative splicing of  
the carboxyl-terminal tails";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94324942; PubMed=8048929;  
RX Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;  
RA "cDNA cloning and functional expression of a human monocyte  
chemoattractant protein 1 receptor";  
RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;  
RX Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;  
RA "Organization and differential expression of the human monocyte  
chemoattractant protein 1 receptor gene. Evidence for the role of the  
carboxyl-terminal tail in receptor trafficking";  
RL J. Biol. Chem. 272:1038-1045(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RX Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RX Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
RX Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,  
RX Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
RX Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
RX Sagripanti J.L.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GIU-355.  
RX Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,  
RX Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;  
RT "SeattlesNPB, NHLBI HL66682 program for genomic applications, UW-  
PHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";

Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

[6]  
 SULFATION OF TYR-26, AND N-GLYCOSYLATION.  
 MEDLINE=20501139; PubMed=11046084;  
 RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,  
 Chakravarty L., Kolatukudy P.E.;  
 RA "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that  
 has tyrosine sulfation in a conserved extracellular N-terminal  
 region.";  
 RT J. Immunol. 165:5295-5303 (2000).  
 CC -1- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
 CC Transduces a signal by increasing the intracellular calcium ions  
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=A;  
 CC IsoId=P41597-1; Sequence=Displayed;  
 CC Name=B;  
 CC IsoId=P41597-2; Sequence=VSP\_001893;  
 CC -1- PTM: N-glycosylated.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U03882; AAL19119.1; -  
 CC EMBL; U03905; AAL19120.1; -  
 CC EMBL; D29984; BAA06253.1; -  
 CC EMBL; U80924; AAC51637.1; -  
 CC EMBL; U80924; AAC51636.1; -  
 CC EMBL; U95626; AAB57791.1; -  
 CC EMBL; U95626; AAB57792.1; -  
 CC EMBL; AF545480; AAN16400.1; -  
 CC PIR; I38450; I38450.  
 CC PIR; JC2443; JC2443.  
 CC PDB; 1KAD; Model; A=1-349.  
 CC PDB; 1KPI; Model; A=1-349.  
 CC Genew; HGNC:1603; CCR2.  
 CC MTM; 601267; -  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0005625; C:soluble fraction; TAS.  
 CC GO; GO:0004950; F:chemokine receptor activity; TAS.  
 CC GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.  
 CC GO; GO:0006968; P:cellular defense response; TAS.  
 CC GO; GO:0006935; P:chemotaxis; TAS.  
 CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.  
 CC GO; GO:0006954; P:inflammatory response; TAS.  
 CC GO; GO:0007259; P:JAK-STAT cascade; TAS.  
 CC GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.  
 CC InterPro; IPR000355; Chkline\_receptor.  
 CC InterPro; IPR000276; GPCR\_Rhodopsin.  
 CC Pfam; PF00001; 7tm\_1; 1.  
 CC PRINTS; PR00237; GPCRHHODOPSIN.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_F1\_1; 1.  
 CC PROSITE; PS00262; G\_PROTEIN\_RECEPTOR\_F2\_1; 1.  
 CC 3D-structure; Alternative splicing; G-protein coupled receptor;  
 CC Glycoprotein; Polymorphism; Sulfation; Transmembrane.  
 CC DOMAIN 1 42 Extracellular (Potential).  
 CC TRANSMEM 43 70 Extracellular (Potential).  
 CC DOMAIN 71 80 Cytoplasmic (Potential).  
 CC TRANSMEM 81 100 2 (Potential).  
 CC DOMAIN 101 114 Extracellular (Potential).  
 CC TRANSMEM 115 136 3 (Potential).  
 CC DOMAIN 137 153 Cytoplasmic (Potential).  
 CC TRANSMEM 154 178 4 (Potential).  
 CC DOMAIN 179 206 Extracellular (Potential).  
 CC

FT	TRANSMEM	207	226	5 (Potential).
FT	DOMAIN	227	243	Cytoplasmic (Potential).
FT	TRANSMEM	244	268	6 (Potential).
FT	DOMAIN	269	285	Extracellular (Potential).
FT	TRANSMEM	286	309	7 (Potential).
FT	DOMAIN	310	374	Cytoplasmic (Potential).
FT	CARBOHYD	14	14	N-linked (GlcNAc. . .) (Potential).
FT	MOD RES	26	26	Sulfotyrosine.
FT	DISULFID	113	190	By similarity.
FT	VARSPLIC	314	374	SLFHIALGCRIALPQKPVCGGPGVRPGKVKVVTQGLLDGR
FT				GKGSIGRAPEASLQDKEGA -> RYLSVFRKHITKRFCK
FT				QCPVFRVETVDGVTSTNTPSTGEQVSAGL (in
FT				isoform B).
FT	VARIANT	64	64	/FTId=VSP_001893
FT				V->I (in dbSNP:1799864).
FT	VARIANT	355	355	/FTId=VAR_014339.
FT				G->E.
FT	VARIANT			/FTId=VAR_014340.
FT	SEQUENCE	374 AA;	41914 MW;	F865E0D39E74CF0F CRC64;
SQ				
	Query Match	100.0%;	Score 1970;	DB 1; Length 374;
	Best Local Similarity	100.0%;	Pred. No. 1e-118;	
	Matches 374;	Conservative	0; Mismatches	0; Indels
				0; Gaps
QY	1	MLSTSRPIRNTNSESGETTFFDYDYGAPCHKFDVKQIGALPLPLYSLVFIFGVGN	60	
DB	1	MLSTSRPIRNTNSESGETTFFDYDYGAPCHKFDVKQIGALPLPLYSLVFIFGVGN	60	
QY	61	MLVVLILNCKLKLCTDIYLLNLAI	120	
DB	61	MLVVLILNCKLKLCTDIYLLNLAI	120	
QY	121	HIGYFGGIPFILLTIDRYLAI	180	
DB	121	HIGYFGGIPFILLTIDRYLAI	180	
QY	181	CQKEDSVYVCGPYFPRGWNFNHIMENILGLVPLLMVTCYSGILKTLRCNEKKRHR	240	
DB	181	CQKEDSVYVCGPYFPRGWNFNHIMENILGLVPLLMVTCYSGILKTLRCNEKKRHR	240	
QY	241	AVRVFTIMIVYFVFWTPYNNIVILLNTFOEFFGLSNCESTSDQATQVTTGLMTHCCI	300	
DB	241	AVRVFTIMIVYFVFWTPYNNIVILLNTFOEFFGLSNCESTSDQATQVTTGLMTHCCI	300	
QY	301	NPIIYAPVGEKPSLFHIALGCRIALPQKPVCGGPGVRPGKVKVVTQGLLDGRGKSI	360	
DB	301	NPIIYAPVGEKPSLFHIALGCRIALPQKPVCGGPGVRPGKVKVVTQGLLDGRGKSI	360	
QY	361	GRAPEASLQDKEGA	374	
DB	361	GRAPEASLQDKEGA	374	
	STANDARD;	PRT;	360 AA.	
	ID_CKCR2	MACMU		
	AC	018793;		
	DT	16-OCT-2001 (Rel. 40, Created)		
	DT	16-OCT-2001 (Rel. 40, Last sequence update)		
	DT	25-OCT-2004 (Rel. 45, Last annotation update)		
	DE	C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)		
	DE	(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).		
	GN	Names=CCR2; Synonyms=CMKBR2;		
	OS	Macaca mulatta (Rhesus macaque).		
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
	OC	Cercopithecoidea; Macaca.		
	OX	NCBI_TaxID=9544;		
	RN	[1]		
	RX	SEQUENCE FROM N.A.		
	RX	MEDLINE=21354176; PubMed=11461684; DOI=10.1089/089922201750290104;		
	RA	Margulies B.J., Hauer D.A., Clements J.E.;		
	RT	"Identification and comparison of eleven rhesus macaque chemokine		



RT receptors. ";  
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
 CC Transduces a signal by increasing the intracellular calcium ions  
 CC level.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=B;  
 CC IsoId=O18793-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoId=O18793-2; Sequence=Not described;  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF013958; AAD11572.1; -;  
 DR InterPro; IPR002237; CC 2\_receptor.  
 DR InterPro; IPR000355; Chem\_kine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G PROTEIN RECP F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW Alternative splicing; G-protein coupled receptor; Glycoprotein;  
 KW Sulfation; Transmembrane.  
 FT DOMAIN 1 42 Extracellular (Potential).  
 FT TRANSMEM 43 70 1 (Potential).  
 FT DOMAIN 71 80 Cytoplasmic (Potential).  
 FT TRANSMEM 81 100 2 (Potential).  
 FT DOMAIN 101 114 Extracellular (Potential).  
 FT TRANSMEM 115 136 3 (Potential).  
 FT DOMAIN 137 153 Cytoplasmic (Potential).  
 FT TRANSMEM 154 178 4 (Potential).  
 FT DOMAIN 179 206 Extracellular (Potential).  
 FT TRANSMEM 207 226 5 (Potential).  
 FT DOMAIN 227 243 Cytoplasmic (Potential).  
 FT TRANSMEM 244 268 6 (Potential).  
 FT DOMAIN 269 285 Extracellular (Potential).  
 FT TRANSMEM 286 309 7 (Potential).  
 FT DOMAIN 310 360 Cytoplasmic (Potential).  
 FT CARBOHYD 14 14 N-linked (GlcNAc...) (Potential).  
 FT MOD\_RES 26 26 Sulfotyrosine (By similarity).  
 FT DISULFID 113 190 By similarity.  
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCB913FE9F CRC64;  
 Query Match 82.0%; Score 1614.5; DB 1; Length 360;  
 Best Local Similarity 96.6%; Pred. No. 6.1e-96;  
 Matches 308; Conservative 4; Mismatches 4; Indels 3; Gaps 1;  
 QY 1 MLSTSRFRIRNTNSESBEVTFDFDYDGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60  
 DB 1 MLSTSRFRIRNTNSESBEVTFDFDYDGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60  
 QY 61 MLVVLILINCKKLCITDIYLLNLAISDLPLITPLWAHSAANEVFGNAMCKLFTGLY 120  
 DB 61 MLVVLILINCKKLCITDIYLLNLAISDLPLITPLWAHSAANEVFGNAMCKLFTGLY 120  
 QY 121 HIGVFGIIPFILLTIDRYLAIVHAVFALKARTTFTGVTSTIWLVAVASVPGIIFTK 180  
 DB 121 HIGVFGIIPFILLTIDRYLAIVHAVFALKARTTFTGVTSTIWLVAVASVPGIIFTK 180  
 QY 181 CQKEDSVVCPYFPRGWNPHITMRNLGLVPLLIWVICYSGLIKTLRCRNEKRRH 240  
 DB 181 CQKEDSVVCPYFPRGWNPHITMRNLGLVPLLIWVICYSGLIKTLRCRNEKRRH 240  
 QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300

Db 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFR---SLF 316  
 Db 301 NPIIYAFVGEKFRYLSMF 319  
 RESULT 3  
 CKR2\_RAT  
 ID CKR2\_RAT STANDARD; PRT; 373 AA.  
 AC O55193;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 GN C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).  
 GN Name=Ccr2; Synonyms=Cmkbr2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN NCBI\_SEQUENCE FROM N.A.  
 RP STRAIN=Sprague-Dawley;  
 RX MEDLINE=96318173; PubMed=9655467; DOI=10.1016/S0165-5728(98)00005-8;  
 RA Jiang Y., Salafraanca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
 RA defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
 RT "Chemokine receptor expression in cultured glia and rat experimental  
 RT allergic encephalomyelitis";  
 RL J. Neuroimmunol. 86:11-12(1998).  
 CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5  
 CC chemokines. Transduces a signal by increasing the intracellular  
 CC calcium ions level (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and  
 CC macrophages.  
 CC -!- INDUCTION: In animals in which experimental allergic  
 CC encephalomyelitis (EAE) has been induced.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U77349; AAC03242.1; -;  
 DR RGD; 620876; Ccr2.  
 DR InterPro; IPR002237; CC 2\_receptor.  
 DR InterPro; IPR000355; Chem\_kine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G PROTEIN RECP F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 60 Extracellular (Potential).  
 FT TRANSMEM 61 81 Potential.  
 FT DOMAIN 82 91 Cytoplasmic (Potential).  
 FT TRANSMEM 92 112 Potential.  
 FT DOMAIN 113 128 Extracellular (Potential).  
 FT TRANSMEM 129 149 Potential.  
 FT DOMAIN 150 170 Cytoplasmic (Potential).  
 FT TRANSMEM 171 191 Potential.  
 FT DOMAIN 192 220 Extracellular (Potential).  
 FT TRANSMEM 221 241 Potential.  
 FT DOMAIN 242 256 Cytoplasmic (Potential).  
 FT TRANSMEM 257 277 Potential.  
 FT DOMAIN 278 301 Extracellular (Potential).  
 FT TRANSMEM 302 322 Potential.  
 FT DOMAIN 323 373 Cytoplasmic (Potential).

FT DISULFID 126 203 By similarity.  
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;  
 Query Match 68.4%; Score 1346.5; DB 1; Length 373;  
 Best Local Similarity 76.9%; Pred. No. 9.5e-79;  
 Matches 257; Conservative 25; Mismatches 45; Indels 7; Gaps 3;  
 QY 1 MLSTSRFRNTNTEGSEEVTTFFDYDYGAPCHKFDVKQIGAOALLPPLYSLVFIKFGVGN 60  
 DB 14 ILTSHSLFRSROELDEGATTPYDDGEPCHTSVKQIGAWILLPPLYSLVFIKFGVGN 73  
 QY 61 MLVVLILNCKLCKLTDIYLAIVHAFKARVTFTGVTSTWLVAVFASVPGIIFTK 120  
 DB 74 MLVILILNCKLCKLTDIYLAIVHAFKARVTFTGVTSTWLVAVFASVPGIIFTK 133  
 QY 121 HIGYFGGIFPIILLTDRYLAIVHAFKARVTFTGVTSTWLVAVFASVPGIIFTK 180  
 DB 134 HIGYFGGIFPIILLTDRYLAIVHAFKARVTFTGVTSTWLVAVFASVPGIIFTK 193  
 QY 181 COXEDSVYVCGPYFPGRGNWFFHTIMRNILGLVPLLMVICYGLKTLALCRNEKKRHR 240  
 DB 194 SEQDDOHTCGPFTTWNKQFQIMRNILSLIPLLVWVICYGLKTLALCRNEKKRHR 253  
 QY 241 AVRVFTIMVYFLFWTPYNNIVILANTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 DB 254 AVRLFAIMVYFLFWTPYNNIVILANTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 313  
 QY 301 NPIIYAPVGBKFR---SLF---HIALG-CRIAPL 327  
 DB 314 NPIIYAPVGBKFRYLSIFPRKRIAKNLCKQCPV 347

## RESULT 4

CKR2\_MOUSE STANDARD; PRT; 373 AA.  
 AC PS1683; Q61172;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)  
 GN (JE/FIC receptor) (MCP-1 receptor).  
 GE Names=Ccr2; Synonyms=Cmkbr2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;  
 RX Boring L., Goelling J., Montecarlo F.S., Luis A.J., Tsou C.-L.,  
 RA Charo I.F.;  
 RT "Molecular cloning and functional expression of murine JE (monocyte  
 RT chemottractant protein 1) and murine macrophage inflammatory protein  
 RT 1alpha receptors: evidence for two closely linked C-C chemokine  
 RT receptors on chromosome 9";  
 RL J. Biol. Chem. 271:7551-7558 (1996).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=BALB/c;  
 RX MEDLINE=96216064; PubMed=8662823; DOI=10.1074/jbc.271.20.11603;  
 RA Kurihara T., Bravo R.;  
 RT "Cloning and functional expression of mCCR2, a murine receptor for the  
 RT C-C chemokines JE and FIC";  
 RL J. Biol. Chem. 271:11603-11606 (1996).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=97026720; PubMed=8872898;  
 RX DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR73.3.CO;2-H;  
 RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,  
 RA Post T.W., Gerard C., Dorf M.E.;  
 RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse  
 RT transcriptase-polymerase chain reaction does not detect mRNA for the  
 RT KC or new MCP-1 receptor.";

RL J. Neurosci. Res. 45:382-391 (1996).  
 CC -1- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5  
 CC chemokines. Transduces a signal by increasing the intracellular  
 CC calcium ions level.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,  
 CC but not in nonhematopoietic cell lines.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U47035; AAC52453.1; -;  
 DR EMBL; U51717; AAC52557.1; -;  
 DR EMBL; U56819; AAC52784.1; -;  
 DR GGD; MGI:106185; Ccr2.  
 DR GO; GO:0016493; F-C chemokine receptor activity; IDA.  
 DR GO; GO:0019955; F-cytokine binding; IPL.  
 DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.  
 DR GO; GO:0030097; P:hemoipoiesis; IMP.  
 DR GO; GO:0006959; P:humoral immune response; IMP.  
 DR GO; GO:0006954; P:inflammatory response; IMP.  
 DR GO; GO:0019233; P:perception of pain; IMP.  
 DR GO; GO:0030334; P:regulation of cell migration; IMP.  
 DR InterPro; IPR002237; CC\_2 receptor.  
 DR InterPro; IPR000355; Chkline receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 55 Extracellular (Potential).  
 FT TRANSMEM 56 83 Cytoplasmic (Potential).  
 FT DOMAIN 84 93 Cytoplasmic (Potential).  
 FT TRANSMEM 94 114 Extracellular (Potential).  
 FT DOMAIN 115 127 Extracellular (Potential).  
 FT TRANSMEM 128 149 Cytoplasmic (Potential).  
 FT DOMAIN 150 166 Cytoplasmic (Potential).  
 FT TRANSMEM 167 191 Extracellular (Potential).  
 FT DOMAIN 192 219 Extracellular (Potential).  
 FT TRANSMEM 220 239 Cytoplasmic (Potential).  
 FT DOMAIN 240 256 Cytoplasmic (Potential).  
 FT TRANSMEM 257 281 Extracellular (Potential).  
 FT DOMAIN 282 298 Extracellular (Potential).  
 FT TRANSMEM 299 322 Cytoplasmic (Potential).  
 FT DOMAIN 323 373 By similarity.  
 FT DISULFID 126 203 Y -> H (in Ref. 1).  
 FT CONFLICT 39 39 A -> G (in Ref. 1).  
 FT CONFLICT 184 184 V -> G (in Ref. 1).  
 FT CONFLICT 264 264 V -> G (in Ref. 1).  
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;  
 Query Match 67.6%; Score 1332.5; DB 1; Length 373;  
 Best Local Similarity 76.3%; Pred. No. 7.5e-78;  
 Matches 255; Conservative 26; Mismatches 46; Indels 7; Gaps 3;  
 QY 1 MLSTSRFRNTNTEGSEEVTTFFDYDYGAPCHKFDVKQIGAOALLPPLYSLVFIKFGVGN 60  
 DB 14 ILTSHSLFRSROELDEGATTPYDDGEPCHTSVKQIGAWILLPPLYSLVFIKFGVGN 73  
 QY 61 MLVVLILNCKLCKLTDIYLAIVHAFKARVTFTGVTSTWLVAVFASVPGIIFTK 120  
 DB 74 MLVILILNCKLCKLTDIYLAIVHAFKARVTFTGVTSTWLVAVFASVPGIIFTK 133  
 QY 121 HIGYFGGIFPIILLTDRYLAIVHAFKARVTFTGVTSTWLVAVFASVPGIIFTK 180  
 DB 134 HIGYFGGIFPIILLTDRYLAIVHAFKARVTFTGVTSTWLVAVFASVPGIIFTK 193



```

Qy 196 RG-----WNNFHTMRNLGLVPLLMIVCYSGILKTLRCNEKKHRAVRVIFTIMIV 251
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 FGQYRFKNLETLKMWILGLVPLLVNVICYSGLIKTLRCNEKKHRAVRVIFTIMIV 243
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 252 YFLFWTPYNIIVLLNTQBFGLSNCESTSQLDQATQVTTGLTHGCCINPIIYAFVGEK 311
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 YFLFWTPYNIIVLLNTQBFGLSNCESTSQLDQATQVTTGLTHGCCINPIIYAFVGEK 303
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 312 FRSLSF-----HTA 319
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 304 FRNYLLVFFOKHIA 317
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q68G28 ID Q68G28 PRELIMINARY; PRT; 354 AA.
AC Q68G28;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chemokine (C-C) receptor 5.
DE Names=Chkbr5;
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.Z., Scherch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
[2]
SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC078756; AAH78756.1; -.
DR GO: GO:0004872; P:receptor activity; IEA.
DR InterPro: IPR000923; BlueCu_1.
DR InterPro: IPR002240; CC_5_receptor.
DR InterPro: IPR000355; Chkline receptor.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00196; COPPER_BLUE.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 354 AA; 41081 MW; 4CCBA9A9C4EE985C CRC64;
Query Match 63.3%; Score 1247; DB 2; Length 354;
Best Local Similarity 75.6%; Pred. No. 2.2e-72;

```

```

Matches 233; Conservative 29; Mismatches 40; Indels 6; Gaps 2;
Qy 17 GEEVTFEFDY--GAPCHKFDVKQIQAQLLPYLSLVFIQFVGNMVLVILINCKKLG 74
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 GSPTIYIDISMSAPCKQFNKQIAAQLLPYLSLVFIQFVGNMVLVILINCKKLG 64
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 75 CLTDIYLLMLAISDLLFLTLPLWAHSAANEWVFGNAMCKLFTGLXHYGFGGIFILL 134
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 SMTDIYLFNLAISDLLFLTLPLWAHSAANEWVFGNAMCKLFTGLXHYGFGGIFILL 124
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 135 TIDRYLAIHVAHPALKARTVTFQVTSVITLWVAFASVPDGIIFTCKQKEDSVVCGPYF 194
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 TIDRYLAIHVAHPAIKARTVTFQVTSVITLWVAFASVPDGIIFTCKQKEDSVVCGPYF 184
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 195 P-----RGWNNFHTMRNLGLVPLLMIVCYSGILKTLRCNEKKHRAVRVIFTIMI 250
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 185 PRIQYRFWKHFQTLKMWILGLVPLLVNVICYSGLIKTLRCNEKKHRAVRVIFTIMI 244
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 251 VYFLFWTPYNIIVLLNTQBFGLSNCESTSQLDQATQVTTGLTHGCCINPIIYAFVGE 310
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 VYFLFWTPYNIIVLLNTQBFGLSNCESTSQLDQATQVTTGLTHGCCINPIIYAFVGE 304
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 311 KFRSLFPHI 318
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 305 KFRNYLSV 312
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q9TQT3 ID Q9TQT3 PRELIMINARY; PRT; 339 AA.
AC Q9TQT3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE Names=CCRS;
GN Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=22942991; PubMed=14591567;
RX DOI=10.1128/JVI.77.22.12310-12318.2003;
RA Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,
RA Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,
RA Doms R.W., Marx P., Wolinsky S.M.;
RT "Structure and function of CC-chemokine receptor 5 homologues derived
RT from representative primate species and subspecies of the taxonomic
RT suborders Prosimii and Anthropoidea."
J. Virol. 77:12310-12318(2003).
[2]
SEQUENCE FROM N.A.
RP Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AF162021; AAD47776.1; -.
DR EMBL: AF161934; AAD47691.1; -.
DR EMBL: AF161935; AAD47692.1; -.
DR EMBL: AF161936; AAD47693.1; -.
DR EMBL: AF161937; AAD47694.1; -.
DR EMBL: AF161938; AAD47695.1; -.
DR EMBL: AF161939; AAD47696.1; -.
DR EMBL: AF161940; AAD47697.1; -.
DR EMBL: AF161944; AAD47700.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR00923; BlueCu_1.

```

```
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline_receptor.
DR EMBL; AF161929; AAC47686.1; -.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR02337; GPCR_HODOPSIN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN 1.
DR PROSITE; PS02337; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39055 MW; C1313952B71B50C7 CRC64;

Query Match 63.1%; Score 1244; DB 2; Length 339;
Best Local Similarity 76.6%; Pred. No. 3.3e-72;
Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

QY 24 FDYDYG--APCHKFDVKQIGALLPPLYSLVFIPIFGVGNMLVVLINCKKLCITDIYL 81
DB 3 YDIDYGPSEPCRKIDVKQGAHLLPPLYSMVFLFGVGNMLVVLINCKKLSMTDIYL 62

QY 82 LNLALSLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIILLTIDRYLA 141
DB 63 LNLALSLLFLITVPFWAHYAAGQWDFGNTWCQFLTGLYFPGSGIFFIILLTIDRYLA 122

QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVVCGPYFP--RG 197
DB 123 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIITRSQEGVHYTCSHPFPYQOF 182

QY 198 WNNPHTIMRNILGLVPLLMVICYSGLIKTLRCRNEKKHRAVRVFTIMIVYFLFWT 257
DB 183 WKNFETLKWVILGLVPLLMVICYSGLIKTLRCRNEKKHRAVRVFTIMIVYFLFWA 242

QY 258 PYNIVILLNTFOEPFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLP- 316
DB 243 PYNIVLLNTYQEPFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFVGEKFRNYLA 302

QY 317 -----HIA 319
DB 303 VFFQKHIA 310

RESULT 9
Q9TUV8 PRELIMINARY; PRT; 339 AA.
AC Q9TUV8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN Name=CCR5;
OS Seguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22942991; PubMed=14581567;
RX DOI=10.1128/JVI.77.22.12310-12318.2003;
RA Kunstan K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,
RA Kunstan J., Stanton J., Agui M., Shibata R., Yoder A.D., Pillai S.,
RA Doms R.W., Marx P., Wolinsky S.M.;
RA "Structure and function of CC-chemokine receptor 5 homologues derived
RT from representative primate species and subspecies of the taxonomic
RT suborders Prosimii and Anthropoidea."
RL J. Virol. 77:12310-12318(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agui M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
```

```
CC -! SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -! SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF161929; AAC47686.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; P:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR02337; GPCR_HODOPSIN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN 1.
DR PROSITE; PS02337; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39164 MW; 6A67CF5D22C70C49 CRC64;

Query Match 63.1%; Score 1244; DB 2; Length 339;
Best Local Similarity 77.3%; Pred. No. 3.3e-72;
Matches 238; Conservative 24; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYDYG--APCHKFDVKQIGALLPPLYSLVFIPIFGVGNMLVVLINCKKLCITDIYL 81
DB 3 YDIDYGPSEPCRKIDVKQGAHLLPPLYSMVFLFGVGNMLVVLINCKKPSMTDIYL 62

QY 82 LNLALSLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIILLTIDRYLA 141
DB 63 LNLALSLLFLITVPFWAHYAAGQWDFGNTWCQFLTGLYFPGSGIFFIILLTIDRYLA 122

QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVVCGPYFP--RG 197
DB 123 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIITRSQEGVHYTCSHPFPYQOF 182

QY 198 WNNPHTIMRNILGLVPLLMVICYSGLIKTLRCRNEKKHRAVRVFTIMIVYFLFWT 257
DB 183 WKNFETLKWVILGLVPLLMVICYSGLIKTLRCRNEKKHRAVRVFTIMIVYFLFWA 242

QY 258 PYNIVILLNTFOEPFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLP- 316
DB 243 PYNIVLLNTYQEPFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFVGEKFRNYLV 302

QY 317 -----HIA 319
DB 303 VFFQKHIA 310

RESULT 10
Q6WN98 PRELIMINARY; PRT; 352 AA.
AC Q6WN98
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CC chemokine receptor 5.
GN Name=ccr5;
OS Callithrix humeralifera (Tassel-eared marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=52232;
RN [1]
RP SEQUENCE FROM N.A.
RA Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RA Seunanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
RT "CCR5 chemokine receptor gene evolution in new world monkeys
RT (Platyrrhini, Primates): implication on resistance to lentiviruses."
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
```

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AY278745; AAQ20013.1; -.  
 DR EMBL; AY278744; AAQ20012.1; -.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.  
 DR GO; GO:0004872; F: receptor activity; IEA.  
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro; IPR000923; BlueCu.1.  
 DR InterPro; IPR002240; CC 5 receptor.  
 DR InterPro; IPR000355; ChmKine\_receptor.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00657; CCHEMOKINER.  
 DR PRINTS; PR01110; CHEMOKINERS.  
 DR PRINTS; PR00237; GPCRHHODOPS.  
 DR PROSITE; PS00196; COPPER\_BLUE; UNKNOWN 1.  
 DR PROSITE; PS00237; G PROTEIN RECF F1\_1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECF F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 352 AA; 40522 MW; PF0D0A852E553AF5 CRC64;  
 Query Match 63.1%; Score 1244; DB 2; Length 352;  
 Best Local Similarity 76.6%; Pred. No. 3.4e-72;  
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;  
 QY 24 FDYDYG--APCHKFDVKQIGAOQLLPPLYSLVFIFGVGNMLVLLILNCKLKLTIDYL 81  
 DB 10 YDIDYGFSEPCRKIDVKQGAHLLPPLYSVFLFVGFGNMLVLLILNCKLKSMTDIYL 69  
 QY 82 LNLAIISDLLFLITPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGFIILLTIDRYLA 141  
 DB 70 LNLAIISDLIFLFTVPFWAHYAAGWDGNTWCQFLTGLYIGFSGFIILLTIDRYLA 129  
 QY 142 IVHAVFALKARTVTFGVVTSVITMLVAVFASVPGIIFTKQKEDSVVCGPYFP 197  
 DB 130 IVHAVFALKARTVTFGVVTSVITMLVAVFASVPGIIFTKQKEDSVVCGPYFP 189  
 QY 198 WNNFHTIMRNILGLVPLLMVTCYSGILKTLRCNEKRRHRAVRVIFIMIVYFLFWT 257  
 DB 190 WKNFETLKWVILGLVPLLMVTCYSGILKTLRCNEKRRHRAVRVIFIMIVYFLFWA 249  
 QY 258 PYNIVILLNTFOBPFGLNCSSTSLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLF- 316  
 DB 250 PYNIVILLNTYQBFGLNCSNRLDQAMQVTTGLMTHCCNPIIYAFVGEKFRSLF 309  
 QY 317 -----HIA 319  
 DB 310 VFFQKHIA 317  
 RESULT 11  
 Q9MZA0 PRELIMINARY; PRT; 352 AA.  
 AC Q9MZA0  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CC chemokine receptor 5 (Chemokine receptor CCR5).  
 GN Name=CCR5; Synonyms=ccr5;  
 OS Callithrix jacchus (Common marmoset).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.  
 OX NCBI\_TaxID=9483;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20317091; PubMed=10747879; DOI=10.1074/jbc.M000169200;  
 RA Mummidi S., Bamehad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,  
 RA Begum K., Galvis M.C., Kosteki V., Valente A.J., Murthy K.K.,  
 RA Hargu L., Dolan J.S., Allan J.S., Ahuja S.K.;  
 RT "Evolution of human and non-human primate CC chemokine receptor 5 gene  
 and mRNA. Potential roles for haplotype and mRNA diversity,"

RT differential haplotype-specific transcriptional activity, and altered  
 RT transcription factor binding to polymorphic nucleotides in the  
 RT pathogenesis of HIV-1 and simian immunodeficiency virus.;  
 RL J. Biol. Chem. 275:18946-18961(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22174698; PubMed=12186836;  
 RA LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;  
 RT "Blockade of HIV-1 infection of New World monkey cells occurs  
 RT primarily at the stage of virus entry";  
 RL J. Exp. Med. 196:431-445(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,  
 RA Seanez H.N., Russo C.A.M., Tamuri A., Soares M.A.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX Zhang Y., Ryder O.A., Zhang Y.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AF252554; AAF87984.1; -.  
 DR EMBL; AF452614; AAN14530.1; -.  
 DR EMBL; AY278743; AAQ20011.1; -.  
 DR EMBL; AF177878; AAK43361.1; -.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.  
 DR GO; GO:0004872; F: receptor activity; IEA.  
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro; IPR000923; BlueCu.1.  
 DR InterPro; IPR002240; CC 5 receptor.  
 DR InterPro; IPR000355; ChmKine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00657; CCHEMOKINER.  
 DR PRINTS; PR01110; CHEMOKINERS.  
 DR PRINTS; PR00237; GPCRHHODOPS.  
 DR PROSITE; PS00196; COPPER\_BLUE; UNKNOWN 1.  
 DR PROSITE; PS00237; G PROTEIN RECF F1\_1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECF F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 352 AA; 40465 MW; PF0D0A8D06F7B8F5 CRC64;  
 Query Match 63.1%; Score 1244; DB 2; Length 352;  
 Best Local Similarity 76.8%; Pred. No. 3.4e-72;  
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;  
 QY 24 FDYDYG--APCHKFDVKQIGAOQLLPPLYSLVFIFGVGNMLVLLILNCKLKLTIDYL 81  
 DB 10 YDIDYGFSEPCRKIDVKQGAHLLPPLYSVFLFVGFGNMLVLLILNCKLKSMTDIYL 69  
 QY 82 LNLAIISDLLFLITPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGFIILLTIDRYLA 141  
 DB 70 LNLAIISDLIFLFTVPFWAHYAAGWDGNTWCQFLTGLYIGFSGFIILLTIDRYLA 129  
 QY 142 IVHAVFALKARTVTFGVVTSVITMLVAVFASVPGIIFTKQKEDSVVCGPYFP 197  
 DB 130 IVHAVFALKARTVTFGVVTSVITMLVAVFASVPGIIFTKQKEDSVVCGPYFP 189  
 QY 198 WNNFHTIMRNILGLVPLLMVTCYSGILKTLRCNEKRRHRAVRVIFIMIVYFLFWT 257  
 DB 190 WKNFETLKWVILGLVPLLMVTCYSGILKTLRCNEKRRHRAVRVIFIMIVYFLFWA 249  
 QY 258 PYNIVILLNTFOBPFGLNCSSTSLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLF- 316  
 DB 250 PYNIVILLNTYQBFGLNCSNRLDQAMQVTTGLMTHCCNPIIYAFVGEKFRSLF 309  
 QY 317 -----HIA 319  
 DB 310 VFFQKHIA 317



```

QY 195 PRG-----WNNFHTMRNIGLVLPFLIMVICYSGILKTLRCRNEKKRRAVRVIFTIMI 250
Db 185 PHQYHFWKSFQTLKMWILSLILPLVMIICYSGLHTLFCRNEKKRRAVRLIFAIMI 244

QY 251 VYFLFWTPYNNIVLLNTFQBFGLSNCESSQDQATQVTTETLGMTHCCINPIIYAPVGE 310
Db 245 VYFLFWTPYNNIVLLNTFQBFGLSNCESSQDQATQVTTETLGMTHCCINPIIYAPVGE 304

QY 311 KPRSLPHI 318
Db 305 KFRSLSV 312

RESULT 13
Q9TQV5 PRELIMINARY; PRT; 339 AA.
AC Q9TQV5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN Name=CCRS5;
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22942991; PubMed=14581567;
RX DOI=10.1128/JVI.77.22.12310-12318.2003;
RA Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,
RA Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,
RA Doms R.W., Marx P., Wolinsky S.M.;
RT "Structure and function of CC-chemokine receptor 5 homologues derived
RT from representative primate species and subspecies of the taxonomic
RT suborders Prosimii and Anthropoidea.";
RT J. Virol. 77:12310-12318(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF161931; AAD47688.1; -
DR EMBL; AF161925; AAD47682.1; -
DR EMBL; AF161926; AAD47683.1; -
DR EMBL; AF161923; AAD47680.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000923; BlueCu.1.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chkline receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1.
FT NON_TER 339.
FT NON_TER 339.
SQ SEQUENCE 339 AA; 39081 MW; 6B79D05D22C70032 CRC64;

Query Match 63.1%; Score 1243; DB 2; Length 339;
Best Local Similarity 76.9%; Pred. No. 3.8e-72;
Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;

```

```

QY 24 FDYDYG--APCHKFDVKQIGAOQLPPLYSLVIFGFGVGNMLVVLILINCKKLCITDIYL 81
Db 3 YDIDYGPSEPCRKIDVKQGAHLLPPLYSVMVLFVFGVGNMLVVLILINCKRPSMTDIYL 62

QY 82 LNLAIADLLFLITLPLWAHSAANEWFVGNAMCKLFTGLYHIGYFGGIFFTLLITIDRYLA 141
Db 63 LNLAIADLLFLITVFPWAHYAAGQWDFGNTMCOFLTGLYFIFGFGGIFFTLLITIDRYLA 122

QY 142 IVHAVFALKARTVTFGVVTSVITLWAVPASVPGIIFTKCKEDSVVVCQPYPRG--- 197
Db 123 IVHAVFALKARTVTFGVVTSVITLWAVPASLPGIIFTSKQEGYHYTCSPHFPFGQYQF 182

QY 198 WNNFHTMRNIGLVLPFLIMVICYSGILKTLRCRNEKKRRAVRVIFTIMIYVFLFWT 257
Db 183 WKNFETLKWVILGLVLPFLIMVICYSGILKTLRCRNEKKRRAVRLIFTIMIVYFLFWA 242

QY 258 PYNIVILLNTFQBFGLSNCESSQDQATQVTTETLGMTHCCINPIIYAVGKFRSLF- 316
Db 243 PYNIVILLNTYQBFGLNCCSSNRDLQAMQVTTETLGMTHCCVNPPIIYAFVGEKFRNLY 302

QY 317 -----HIA 319
Db 303 VFFQKHIA 310

RESULT 14
Q9SNCA PRELIMINARY; PRT; 352 AA.
ID Q9SNCA;
AC Q9SNCA;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C-C chemokine receptor 5.
GN Name=CCRS5;
OS Ateles geoffroyi (Black-handed spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
OX NCBI_TaxID=9509;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF177885; AAK43368.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000923; BlueCu.1.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chkline receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40440 MW; F0A686CB4FE3964B CRC64;

Query Match 63.1%; Score 1243; DB 2; Length 352;
Best Local Similarity 76.6%; Pred. No. 4e-72;
Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

QY 24 FDYDYG--PCHKFDVKQIGAOQLPPLYSLVIFGFGVGNMLVVLILINCKKLCITDIYL 81
Db 10 YDIDYGPSEPCRKIDVKQGAHLLPPLYSVMVLFVFGVGNMLVVLILINCKRPSMTDIYL 69

QY 82 LNLAIADLLFLITLPLWAHSAANEWFVGNAMCKLFTGLYHIGYFGGIFFTLLITIDRYLA 141

```



```
Db 70 LNLAISSLFLFTVFFWAHVAAGQMDFGNTMCQPLTGLYFGPSGIFFIILLTIDRYLA 129
Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVVCVGPYPRG---- 197
Db 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVVCVGPYPRG---- 197
Qy 198 WNNFHTIMRNILGLVPLLMVICYSIGILKTLRCRNEKKRHRVAVRVIPTIMIYVFLFWT 257
Db 190 WKNFETLKMVILGLVPLLMVICYSIGILKTLRCRNEKKRHRVAVRVIPTIMIYVFLFWA 249
Qy 258 PYNIVILLNTFOBFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLF- 316
Db 250 PYNIVLLNTYQBFGLNCCSSNRLDQAMQVTTGLMTHCCVNPPIIYAFVGEKFRNVLV 309
Qy 317 -----HIA 319
Db 310 VFFQKHIA 317
```

## RESULT 15

```
Q6WN93
ID Q6WN93 PRELIMINARY; PRT; 352 AA.
AC Q6WN93;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE CC chemokine receptor 5.
GN Name=ccr5;
OS Leontopithecus chrysopygus (Gold-and-black lion tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Leontopithecus.
OX NCBI_TaxID=58710;
RN [1]
RP SEQUENCE FROM N.A.
RA Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RA Suanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY278750; AAQ20018.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000923; BlueCh1.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40437 MW; 5EC1884238503783 CRC64;
```

Query Match 63.0%; Score 1241; DB 2; Length 352;  
Best Local Similarity 76.3%; Pred. No. 5.3e-72;  
Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;

```
Qy 24 FDYDGA--PCHKFDVQIQAGQLLPPLYSLSVIFGFGVGNMLVVLINCKLKCLTDIYL 81
Db 10 YDIDYGASBFCRKIDVRQMGHLLPPLYSVMVFLFGFGVGNMLVVLINCKRPSMTDIYL 69
Qy 82 LNLAISSLFLFTVFFWAHVAAGQMDFGNTMCQPLTGLYFGPSGIFFIILLTIDRYLA 141
Db 70 LNLAISSLFLFTVFFWAHVAAGQMDFGNTMCQPLTGLYFGPSGIFFIILLTIDRYLA 129
```

Search completed: June 9, 2005, 16:48:06  
Job time : 117.165 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:37:43 ; Search time 31.0817 Seconds  
(without alignments)  
898.236 Million cell updates/sec

Title: US-10-791-166-2

Perfect score: 1970

Sequence: 1 MLSTSRFRIRNTNESGEV.....GKSGSIGRAPEASLDQKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1970	100.0	374	1	US-08-450-393A-2
2	1970	100.0	374	3	US-08-446-669-2
3	1970	100.0	374	4	US-10-039-659A-14
4	1970	100.0	374	4	US-09-625-573-2
5	1970	100.0	374	5	PCT-US95-00476-2
6	1970	100.0	387	4	US-09-949-016-11222
7	1823	92.5	344	3	US-08-466-343D-9
8	1823	92.5	344	4	US-09-502-783A-9
9	1727.5	87.7	329	4	US-09-502-783A-9
10	1727.5	87.7	329	4	US-09-339-912A-9
11	1727.5	87.7	329	4	US-09-195-662A-9
12	1651.5	83.8	360	1	US-08-450-393A-4
13	1651.5	83.8	360	3	US-08-446-669-4
14	1651.5	83.8	360	3	US-09-045-583-50
15	1651.5	83.8	360	4	US-09-534-185-50
16	1651.5	83.8	360	4	US-09-131-827A-2
17	1651.5	83.8	360	4	US-09-625-573-4
18	1651.5	83.8	360	5	PCT-US95-00476-4
19	1651.5	83.8	377	4	US-09-949-016-11221
20	1650.5	83.8	360	4	US-09-131-827A-20
21	1645.5	83.5	360	4	US-08-833-752-7
22	1645.5	83.5	360	4	US-09-938-719-7
23	1645.5	83.5	360	4	US-09-939-226B-7
24	1645.5	83.5	360	4	US-09-826-509-473
25	1614.5	82.0	360	3	US-09-045-583-51
26	1614.5	82.0	360	4	US-09-534-185-51
27	1589.5	80.7	347	1	US-08-461-244-3

28 1236 62.7 352 3 US-09-517-605-5 Sequence 5, Appli  
29 1234 62.6 354 3 US-08-724-984A-2 Sequence 2, Appli  
30 1230 62.4 352 3 US-09-045-583-52 Sequence 52, Appli  
31 1230 62.4 352 4 US-09-534-185-52 Sequence 52, Appli  
32 1224 62.1 352 3 US-09-087-232A-13 Sequence 13, Appli  
33 1224 62.1 352 3 US-08-861-105-14 Sequence 14, Appli  
34 1224 62.1 352 3 US-08-575-967A-2 Sequence 2, Appli  
35 1224 62.1 352 4 US-08-833-752-5 Sequence 5, Appli  
36 1224 62.1 352 4 US-09-502-783A-2 Sequence 2, Appli  
37 1224 62.1 352 4 US-09-796-202-1 Sequence 1, Appli  
38 1224 62.1 352 4 US-09-938-719-5 Sequence 5, Appli  
39 1224 62.1 352 4 US-09-502-784A-2 Sequence 2, Appli  
40 1224 62.1 352 4 US-09-339-912A-2 Sequence 2, Appli  
41 1224 62.1 352 4 US-08-771-276-2 Sequence 2, Appli  
42 1224 62.1 352 4 US-08-771-276-20 Sequence 20, Appli  
43 1224 62.1 352 4 US-09-939-226B-5 Sequence 5, Appli  
44 1224 62.1 352 4 US-09-195-662A-2 Sequence 2, Appli  
45 1218 61.8 352 4 US-09-826-509-477 Sequence 477, App

#### ALIGNMENTS

##### RESULT 1

US-08-450-393A-2  
; Sequence 2, Application US/08450393A  
; Patent No. 5707815  
; GENERAL INFORMATION:  
; APPLICANT: Charo. Israel  
; APPLICANT: Coughlin, Shaun  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; TITLE OF INVENTION: PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,393A  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cserr, Luann  
; REGISTRATION NUMBER: 31,822  
; REFERENCE/DOCKET NUMBER: UCAL-237/0205  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5165  
; TELEFAX: 415-8857-0663  
; TELEX: 380816CooleyPA  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-450-393A-2

Query Match 100.0%; Score 1970; DB 1; Length 374;  
Best Local Similarity 100.0%; Pred. No. 4,3e-150;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRFRIRNTNESGEVTTTFDDYDYGAPCHKFDVKQIGALLPPLYSLVFIFFGVGN 60

Db 1 MLSTSRFRIRNTNESGEVTTTFDDYDYGAPCHKFDVKQIGALLPPLYSLVFIFFGVGN 60



QY 181 COKEDSVVCGPYPRGNNPHTIMRNILGLVPLLLIMVICYSGLIKTLRCRNEKKRHR 240  
 Db 181 COKEDSVVCGPYPRGNNPHTIMRNILGLVPLLLIMVICYSGLIKTLRCRNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFOBFFGLSNCESTSQLDQATQVETLGTWTHCCI 300  
 Db 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFOBFFGLSNCESTSQLDQATQVETLGTWTHCCI 300  
 QY 301 NPIIYAFVGEKFRSLFHIALGCRITAPLOKPVCGGPGVRPGNNKVVTTQGLLDGRGKSKI 360  
 Db 301 NPIIYAFVGEKFRSLFHIALGCRITAPLOKPVCGGPGVRPGNNKVVTTQGLLDGRGKSKI 360  
 QY 361 GRAPEASLQDKEGA 374  
 Db 361 GRAPEASLQDKEGA 374

RESULT 4  
 US-09-625-573-2  
 ; Sequence 2, Application US/09625573  
 ; Patent No. 6730301  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charo, Israel  
 ; Coughlin, Shaun  
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 ; STREET: 5 Palo Alto Square  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94306-2155  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/625,573  
 ; FILING DATE: 25-Jul-2000  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/446,669  
 ; FILING DATE: May 25, 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Neeley, Richard  
 ; REGISTRATION NUMBER: 30,092  
 ; REFERENCE/DOCKET NUMBER: UCAL-237/01US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-843-5000  
 ; TELEFAX: 415-857-0663  
 ; TELEX: 380816COOLEYPA  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 374 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-625-573-2

Query Match 100.0%; Score 1970; DB 4; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-150;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60  
 Db 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60  
 QY 61 MLVVLILINCKKLCITDIYILNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Db 61 MLVVLILINCKKLCITDIYILNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
 QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVTTSVITWLVAVFASVFGIIFTK 180  
 Db 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVTTSVITWLVAVFASVFGIIFTK 180  
 QY 181 COKEDSVVCGPYPRGNNPHTIMRNILGLVPLLLIMVICYSGLIKTLRCRNEKKRHR 240  
 Db 181 COKEDSVVCGPYPRGNNPHTIMRNILGLVPLLLIMVICYSGLIKTLRCRNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFOBFFGLSNCESTSQLDQATQVETLGTWTHCCI 300  
 Db 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFOBFFGLSNCESTSQLDQATQVETLGTWTHCCI 300  
 QY 301 NPIIYAFVGEKFRSLFHIALGCRITAPLOKPVCGGPGVRPGNNKVVTTQGLLDGRGKSKI 360  
 Db 301 NPIIYAFVGEKFRSLFHIALGCRITAPLOKPVCGGPGVRPGNNKVVTTQGLLDGRGKSKI 360  
 QY 361 GRAPEASLQDKEGA 374  
 Db 361 GRAPEASLQDKEGA 374

RESULT 5  
 PCT-US95-00476-2  
 ; Sequence 2, Application PC/TUS9500476  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
 ; TITLE OF INVENTION: PROTEIN RECEPTORS  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Robbins, Berliner & Carson  
 ; STREET: 201 N. Figueroa Street, 5th Floor  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 90012-2628  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/00476  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Berliner, Robert  
 ; REGISTRATION NUMBER: 20,121  
 ; REFERENCE/DOCKET NUMBER: 5555-291  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 310-977-1001  
 ; TELEFAX: 310-977-1003  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 374 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PCT-US95-00476-2

Query Match 100.0%; Score 1970; DB 5; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-150;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60  
 Db 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60  
 QY 61 MLVVLILINCKKLCITDIYILNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Db 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLITDRYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLFTK 180  
Db 121 HIGYFGGIFPIILLITDRYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLFTK 180  
QY 181 CQKEDSVVCGPYFPGRNPHIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240  
Db 181 CQKEDSVVCGPYFPGRNPHIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
Db 241 AVRVIPTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPITYAFVGEKPSLFHIALGCRPIAPLOKPCGPGVRPGKNVKVTTQGLDGRGKSI 360  
Db 301 NPITYAFVGEKPSLFHIALGCRPIAPLOKPCGPGVRPGKNVKVTTQGLDGRGKSI 360  
QY 361 GRAPEASLQDKEGA 374  
Db 361 GRAPEASLQDKEGA 374

## RESULT 6

US-09-949-016-11222  
; Sequence 11222, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11222  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11222

Query Match 100.0%; Score 1970; DB 4; Length 387;  
Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNESGEVTFPDYDYGAPCHKFDVKQIAGALLPPLYSLVIFGFGVN 60  
Db 14 MLSTSRFRIRNTNESGEVTFPDYDYGAPCHKFDVKQIAGALLPPLYSLVIFGFGVN 73  
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120  
Db 74 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 133  
QY 121 HIGYFGGIFPIILLITDRYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLFTK 180  
Db 134 HIGYFGGIFPIILLITDRYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLFTK 193  
QY 181 CQKEDSVVCGPYFPGRNPHIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240  
Db 194 CQKEDSVVCGPYFPGRNPHIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 253  
QY 241 AVRVIPTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
Db 254 AVRVIPTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 313  
QY 301 NPITYAFVGEKPSLFHIALGCRPIAPLOKPCGPGVRPGKNVKVTTQGLDGRGKSI 360

Db 314 NPITYAFVGEKPSLFHIALGCRPIAPLOKPCGPGVRPGKNVKVTTQGLDGRGKSI 373  
QY 361 GRAPEASLQDKEGA 374  
Db 374 GRAPEASLQDKEGA 387

## RESULT 7

US-08-466-343D-9  
; Sequence 9, Application US/08466343D  
; Patent No. 6025154  
; GENERAL INFORMATION:  
; APPLICANT: LI, Yi  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN  
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,343D  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 344 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-466-343D-9

Query Match 92.5%; Score 1823; DB 3; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2.3e-138;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 18 EVVTFPDYDYGAPCHKFDVKQIAGALLPPLYSLVIFGFGVNMLVLLINCKKLCIT 77  
Db 1 EVVTFPDYDYGAPCHKFDVKQIAGALLPPLYSLVIFGFGVNMLVLLINCKKLCIT 60  
QY 78 DIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFPIILLIT 137  
Db 61 DIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFPIILLIT 120  
QY 138 RYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLFTKCKEDSVVCGPYFPG 197  
Db 121 RYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLFTKCKEDSVVCGPYFPG 180  
QY 198 WNNFHTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHRVAVRVIPTIMIVYFLW 257  
Db 181 WNNFHTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHRVAVRVIPTIMIVYFLW 240  
QY 258 PYNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKPSLF 317  
Db 241 PYNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKPSLF 300

; NUMBER OF SEQ ID NOS: 9

QY 138 RYLAIVHAVFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVVVCOPYFPRG 197

Db 106 RYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGPIFPRG 165  
QY 198 WNNFHTIMRNILGLVPLLLIMVTCYSGILKTLRCNEKRRHRAVRVIFTIMIVYFLFWT 257  
Db 166 WNNFHTIMRNILGLVPLLLIMVTCYSGILKTLRCNEKRRHRAVRVIFTIMIVYFLFWT 225  
QY 258 PYNIVILLNTFQBFGLSNCESTSQLDOATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 317  
Db 226 PYNIVILLNTFQBFGLSNCESTSQLDOATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 285  
QY 318 IALGCRITAPLOKPVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 361  
Db 286 IALGCRITAPLOKPVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 329  
RESULT 11  
US-09-195-662A-9  
; Sequence 9, Application US/09195662A  
; Patent No. 6800729  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi  
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10 (CCR5 Receptor)  
; FILE REFERENCE: 1488.1150002  
; CURRENT APPLICATION NUMBER: US/09/195,662A  
; CURRENT FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 08/466,343  
; PRIOR FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Protein  
US-09-195-662A-9  
Query Match 87.7%; Score 1727.5; DB 4; Length 329;  
Best Local Similarity 95.6%; Pred. No. 9.8e-131;  
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;  
QY 18 EEVTFDFDYDYGAPCHKFDVKQIGALLPPLYSILVIFGFVGNMLVLLINCKLKCLT 77  
Db 1 EEVTFDFDYDYGAPCHKFDVKQIGALLPPLYSILVIFGFVGNMLVLLINCKLKCLT 60  
QY 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLTHIGVFGGIFPIILLTID 137  
Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105  
QY 138 RYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGPIFPRG 197  
Db 106 RYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGPIFPRG 165  
QY 198 WNNFHTIMRNILGLVPLLLIMVTCYSGILKTLRCNEKRRHRAVRVIFTIMIVYFLFWT 257  
Db 166 WNNFHTIMRNILGLVPLLLIMVTCYSGILKTLRCNEKRRHRAVRVIFTIMIVYFLFWT 225  
QY 258 PYNIVILLNTFQBFGLSNCESTSQLDOATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 317  
Db 226 PYNIVILLNTFQBFGLSNCESTSQLDOATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 285  
QY 318 IALGCRITAPLOKPVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 361  
Db 286 IALGCRITAPLOKPVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 329

RESULT 12  
US-08-450-393A-4  
; Sequence 4, Application US/08450393A  
; Patent No. 5707815  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; TITLE OF INVENTION: PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,393A  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cseri, Luann  
; REGISTRATION NUMBER: 31,822  
; REFERENCE/DOCKET NUMBER: UCAL-237/02US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5165  
; TELEFAX: 415-8857-0663  
; TELEX: 380816COOLEYPA  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-450-393A-4  
Query Match 83.8%; Score 1651.5; DB 1; Length 360;  
Best Local Similarity 95.5%; Pred. No. 1.3e-124;  
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;  
QY 1 MLSTSRIRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSILVIFGFVGN 60  
Db 1 MLSTSRIRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSILVIFGFVGN 60  
QY 61 MLVLLINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
Db 61 MLVLLINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 180  
Db 121 HIGYFGGIFPIILLTIDRYLAIHVAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPIFPRGNNFHTIMRNILGLVPLLLIMVTCYSGILKTLRCNEKRRH 240  
Db 181 CQKEDSVYVCGPIFPRGNNFHTIMRNILGLVPLLLIMVTCYSGILKTLRCNEKRRH 240  
QY 241 AVRVIITIMVYFLFWTPYNIIVILLNTFQBFGLSNCESTSQLDOATQVTTGLMTHCC 300  
Db 241 AVRVIITIMVYFLFWTPYNIIVILLNTFQBFGLSNCESTSQLDOATQVTTGLMTHCC 300  
QY 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327  
Db 301 NPIIYAFVGEKFRRLSVFPRKHITKRFCKQCPV 334  
RESULT 13  
US-08-446-669-4  
; Sequence 4, Application US/08446669  
; Patent No. 6132987  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; APPLICANT: Coughlin, Shaun  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; APPLICANT: PROTEIN RECEPTORS



; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 ; STREET: 5 Palo Alto Square  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94306-2155  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/446,669  
 ; FILING DATE: May 25, 1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Neeley, Richard  
 ; REGISTRATION NUMBER: 30,092  
 ; REFERENCE/DOCKET NUMBER: UCAL-237/0105  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-843-5000  
 ; TELEFAX: 415-857-0663  
 ; TELEX: 380816COOLEYPA  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 360 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-446-669-4

Query Match 83.8%; Score 1651.5; DB 3; Length 360;  
 Best Local Similarity 95.5%; Pred. No. 1.3e-124;  
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

QY	1	MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFFGVGN	60
Db	1	MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFFGVGN	60
QY	61	MLVVLILINCKKLCUETDIYLLNLAISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLCUETDIYLLNLAISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY	120
QY	121	HIGYFGGIFILLITIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK	180
Db	121	HIGYFGGIFILLITIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK	180
QY	181	CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCRNEKKRHR	240
QY	241	AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFGLSNCESTSQLDOATQVTTGLMTHCCI	300
Db	241	AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFGLSNCESTSQLDOATQVTTGLMTHCCI	300
QY	301	NPITIAFVGEKFR---SLF---HIALG-CRIAPL 327	
Db	301	NPITIAFVGEKFR---SLF---HIALG-CRIAPL 327	

RESULT 14  
 US-09-583-50  
 ; Sequence 50, Application US/09045583  
 ; Patent No. 6287805  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Graham, Gerard J. et al.  
 ; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
 ; NUMBER OF SEQUENCES: 56  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street

; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/045,583  
 ; FILING DATE: 20-MAR-98  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mandragoras, Amy E.  
 ; REGISTRATION NUMBER: 36,207  
 ; REFERENCE/DOCKET NUMBER: MNI-044  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617)227-7400  
 ; TELEFAX: (617)742-4214  
 ; INFORMATION FOR SEQ ID NO: 50:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 360 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 ; US-09-045-583-50

Query Match 83.8%; Score 1651.5; DB 3; Length 360;  
 Best Local Similarity 95.5%; Pred. No. 1.3e-124;  
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

QY	1	MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFFGVGN	60
Db	1	MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFFGVGN	60
QY	61	MLVVLILINCKKLCUETDIYLLNLAISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLCUETDIYLLNLAISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY	120
QY	121	HIGYFGGIFILLITIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK	180
Db	121	HIGYFGGIFILLITIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK	180
QY	181	CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCRNEKKRHR	240
QY	241	AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFGLSNCESTSQLDOATQVTTGLMTHCCI	300
Db	241	AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFGLSNCESTSQLDOATQVTTGLMTHCCI	300
QY	301	NPITIAFVGEKFR---SLF---HIALG-CRIAPL 327	
Db	301	NPITIAFVGEKFR---SLF---HIALG-CRIAPL 327	

RESULT 15  
 US-09-534-185-50  
 ; Sequence 50, Application US/09534185  
 ; Patent No. 6403767  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Graham, Gerard J. et al.  
 ; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
 ; Heptahelical Receptor Superfamily and Uses  
 ; Therefor  
 ; NUMBER OF SEQUENCES: 56  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,185  
FILING DATE: 24-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,583  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-09-534-185-50

Query Match 83.8%; Score 1651.5; DB 4; Length 360;  
Best Local Similarity 95.5%; Pred. No. 1.3e-124;  
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;  
QY 1 MLSTSRFRIRNTNESGEVTFDYDGAPCHKFDVKQIGAOQLPPLYSLVFIQGVGN 60  
DB 1 MLSTSRFRIRNTNESGEVTFDYDGAPCHKFDVKQIGAOQLPPLYSLVFIQGVGN 60  
QY 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
DB 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAFPALKARTVTFGVTSVITWLVAFASVPGIIFTK 180  
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAFPALKARTVTFGVTSVITWLVAFASVPGIIFTK 180  
QY 181 COKEDSVYVCGPYFPRGMNPFTHMNLGLVPLLMVICYSGILKTLRCRNEKKRHR 240  
DB 181 COKEDSVYVCGPYFPRGMNPFTHMNLGLVPLLMVICYSGILKTLRCRNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFOFFGLSNCESTSOLDQATQVETILGMTHCCI 300  
DB 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFOFFGLSNCESTSOLDQATQVETILGMTHCCI 300  
QY 301 NPITYAFVGEKFR---SLF---HIALG-CRIAPL 327  
DB 301 NPITYAFVGEKFRYLSVFFRKHTKRFCKQCPV 334

Search completed: June 9, 2005, 16:50:10  
Job time : 32.0817 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1970	100.0	374	10	US-09-893-512-13	Sequence 1
2	1970	100.0	374	14	US-10-039-659-14	Sequence 1
3	1970	100.0	374	14	US-10-239-423-63	Sequence 6
4	1970	100.0	374	16	US-10-754-071-14	Sequence 1
5	1970	100.0	374	16	US-10-741-601-287	Sequence 2
6	1970	100.0	374	16	US-10-791-592-2	Sequence 2
7	1970	100.0	374	16	US-10-791-166-2	Sequence 2
8	1970	100.0	374	17	US-10-759-860-14	Sequence 1
9	1970	100.0	374	17	US-10-799-736-13	Sequence 1
10	1823	92.5	344	9	US-09-779-879A-9	Sequence 9,
11	1823	92.5	344	9	US-09-779-880A-9	Sequence 9,

Db 61 MLVVLILINCKKLKCLTDIYLLNLAIISDLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
Qy 121 HIGYFGGIFPIILLTIDRYLAIVHAFVPAKARTVTEGVVTSVITLWVAVPASVPGIIFTK 180  
Db 121 HIGYFGGIFPIILLTIDRYLAIVHAFVPAKARTVTEGVVTSVITLWVAVPASVPGIIFTK 180  
Qy 181 CQKEDSVVCGPYFPRGWNFNHTIMRNILGLVPLLIWVICYSGILKTLRLCRNEKKRHR 240  
Db 181 CQKEDSVVCGPYFPRGWNFNHTIMRNILGLVPLLIWVICYSGILKTLRLCRNEKKRHR 240  
Qy 241 AVRVIETIMIVYFLEWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
Db 241 AVRVIETIMIVYFLEWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
Qy 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVRPGKNVKTQTQGLLDGRGKSKI 360  
Db 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVRPGKNVKTQTQGLLDGRGKSKI 360  
Qy 361 GRAPEASLQDKEGA 374  
Db 361 GRAPEASLQDKEGA 374

RESULT 2

US-10-039-659-14  
; Sequence 14, Application US/10039659  
; Publication No. US20030018167A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Wei  
; Gish, Kurt C.  
; Schall, Thomas J.  
; Vicari, Alain P.  
; Zlotnick, Albert  
; TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/039,659  
; FILING DATE: 03-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/887,977  
; FILING DATE: 03-JUL-1997  
; APPLICATION NUMBER: US 60/021,644  
; FILING DATE: 05-JUL-1996  
; APPLICATION NUMBER: US 60/028,329  
; FILING DATE: 11-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0589K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9192  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-039-659-14  
Query Match 100.0%; Score 1970; DB 14; Length 374;  
Best Local Similarity 100.0%; Pred. No. 3.4e-163;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60  
Db 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60  
Qy 61 MLVVLILINCKKLKCLTDIYLLNLAIISDLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
Db 61 MLVVLILINCKKLKCLTDIYLLNLAIISDLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
Qy 121 HIGYFGGIFPIILLTIDRYLAIVHAFVPAKARTVTEGVVTSVITLWVAVPASVPGIIFTK 180  
Db 121 HIGYFGGIFPIILLTIDRYLAIVHAFVPAKARTVTEGVVTSVITLWVAVPASVPGIIFTK 180  
Qy 181 CQKEDSVVCGPYFPRGWNFNHTIMRNILGLVPLLIWVICYSGILKTLRLCRNEKKRHR 240  
Db 181 CQKEDSVVCGPYFPRGWNFNHTIMRNILGLVPLLIWVICYSGILKTLRLCRNEKKRHR 240  
Qy 241 AVRVIETIMIVYFLEWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
Db 241 AVRVIETIMIVYFLEWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
Qy 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVRPGKNVKTQTQGLLDGRGKSKI 360  
Db 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVRPGKNVKTQTQGLLDGRGKSKI 360  
Qy 361 GRAPEASLQDKEGA 374  
Db 361 GRAPEASLQDKEGA 374

RESULT 3

US-10-239-423-63  
; Sequence 63, Application US/10239423  
; Publication No. US20030186889A1  
; GENERAL INFORMATION:  
; APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ADERMAN, Knut;  
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj  
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the  
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammatory Diseases,  
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,  
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine  
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction  
; FILE REFERENCE: 022217us  
; CURRENT APPLICATION NUMBER: US/10/239,423  
; CURRENT FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: DE10016013.1  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 63  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies  
US-10-239-423-63

Query Match 100.0%; Score 1970; DB 14; Length 374;  
Best Local Similarity 100.0%; Pred. No. 3.4e-163;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60  
Db 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60  
Qy 61 MLVVLILINCKKLKCLTDIYLLNLAIISDLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120

```

Db      61  MLVLLILNCKKLCITDIYLLNLAISDLLFLITPLMAHSAANEWVFGNAMCKLFTGLY 120
Qy      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Db      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Qy      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240
Db      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240
Qy      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLTGMTHCCI 300
Db      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLTGMTHCCI 300
Qy      301  NPIIYAVGKFRSLFHIALGCRITAPLQKPVCGGPGVRPGKNVKTQGLLDGRGKSKI 360
Db      301  NPIIYAVGKFRSLFHIALGCRITAPLQKPVCGGPGVRPGKNVKTQGLLDGRGKSKI 360
Qy      361  GRAPEASLQDKEGA 374
Db      361  GRAPEASLQDKEGA 374

```

RESULT 4

```

US-10-754-071-14
; Sequence 14, Application US/10754071
; Publication No. US20040137578A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Chemokine TECK Polypeptides
; FILE REFERENCE: DK0589KIC US
; CURRENT APPLICATION NUMBER: US/10/754,071
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 10/039,659
; PRIOR FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-754-071-14

```

```

Query Match      100.0%; Score 1970; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MLSTSRSRFRINTNESGEEVTFDFDYDGAPCHKFDVKQIGAQLLPPLYSILVFIFFGVGN 60
Db      1  MLSTSRSRFRINTNESGEEVTFDFDYDGAPCHKFDVKQIGAQLLPPLYSILVFIFFGVGN 60
Qy      61  MLVLLILNCKKLCITDIYLLNLAISDLLFLITPLMAHSAANEWVFGNAMCKLFTGLY 120
Db      61  MLVLLILNCKKLCITDIYLLNLAISDLLFLITPLMAHSAANEWVFGNAMCKLFTGLY 120
Qy      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Db      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Qy      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240

```

```

Db      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240
Qy      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLTGMTHCCI 300
Db      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLTGMTHCCI 300
Qy      301  NPIIYAVGKFRSLFHIALGCRITAPLQKPVCGGPGVRPGKNVKTQGLLDGRGKSKI 360
Db      301  NPIIYAVGKFRSLFHIALGCRITAPLQKPVCGGPGVRPGKNVKTQGLLDGRGKSKI 360
Qy      361  GRAPEASLQDKEGA 374
Db      361  GRAPEASLQDKEGA 374

```

RESULT 5

```

US-10-741-601-287
; Sequence 287, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 287
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-287

```

```

Query Match      100.0%; Score 1970; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MLSTSRSRFRINTNESGEEVTFDFDYDGAPCHKFDVKQIGAQLLPPLYSILVFIFFGVGN 60
Db      1  MLSTSRSRFRINTNESGEEVTFDFDYDGAPCHKFDVKQIGAQLLPPLYSILVFIFFGVGN 60
Qy      61  MLVLLILNCKKLCITDIYLLNLAISDLLFLITPLMAHSAANEWVFGNAMCKLFTGLY 120
Db      61  MLVLLILNCKKLCITDIYLLNLAISDLLFLITPLMAHSAANEWVFGNAMCKLFTGLY 120
Qy      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Db      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Qy      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240
Db      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240
Qy      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLTGMTHCCI 300
Db      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLTGMTHCCI 300
Qy      301  NPIIYAVGKFRSLFHIALGCRITAPLQKPVCGGPGVRPGKNVKTQGLLDGRGKSKI 360
Db      301  NPIIYAVGKFRSLFHIALGCRITAPLQKPVCGGPGVRPGKNVKTQGLLDGRGKSKI 360
Qy      361  GRAPEASLQDKEGA 374
Db      361  GRAPEASLQDKEGA 374

```

RESULT 6

```

US-10-791-592-2
; Sequence 2, Application US/10791592
; Publication No. US20040219644A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Charo, Israel
; Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS
;
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/791,592
; FILING DATE: 01-Mar-2004
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,573
; FILING DATE: 25-Jul-2000
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-791-592-2

```

```

Query Match 100.0%; Score 1970; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60
DB 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60

QY 61 MLVVILINCKLKCLTDIYLLNLAISDLLFLITPLWHAASAANWVFGNACKLFTGLY 120
DB 61 MLVVILINCKLKCLTDIYLLNLAISDLLFLITPLWHAASAANWVFGNACKLFTGLY 120

QY 121 HIGVFGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK 180
DB 121 HIGVFGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK 180

QY 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVPLLMVWICYSGLKTLRCNKKRHR 240
DB 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVPLLMVWICYSGLKTLRCNKKRHR 240

QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300

QY 301 NPIIYAVGKFKSLFHIALGCRITAPLQKPCGPGVRPGKNVKTQGLDGRGKSI 360
DB 301 NPIIYAVGKFKSLFHIALGCRITAPLQKPCGPGVRPGKNVKTQGLDGRGKSI 360

QY 361 GRAPEASLQDKEGA 374
DB 361 GRAPEASLQDKEGA 374

```

```

Db 361 GRAPEASLQDKEGA 374

RESULT 7
US-10-791-166-2
; Sequence 2, Application US/10791166
; Publication No. US20040223968A1
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS
;
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/791,166
; FILING DATE: 01-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,573
; FILING DATE: 25-Jul-2000
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-791-166-2

```

```

Query Match 100.0%; Score 1970; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60
DB 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60

QY 61 MLVVILINCKLKCLTDIYLLNLAISDLLFLITPLWHAASAANWVFGNACKLFTGLY 120
DB 61 MLVVILINCKLKCLTDIYLLNLAISDLLFLITPLWHAASAANWVFGNACKLFTGLY 120

QY 121 HIGVFGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK 180
DB 121 HIGVFGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK 180

QY 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVPLLMVWICYSGLKTLRCNKKRHR 240
DB 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVPLLMVWICYSGLKTLRCNKKRHR 240

QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300

```

Db 241 AVRVIPTIMIVYFLWTPYNIIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 Qy 301 NPITYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLDGRGKSKI 360  
 Db 301 NPITYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLDGRGKSKI 360  
 Qy 361 GRAPEASLQDKEGA 374  
 Db 361 GRAPEASLQDKEGA 374  
 RESULT 8  
 US-10-759-860-14  
 ; Sequence 14, Application US/10759860  
 ; Publication No. US2005007490A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Wei  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Schall, Thomas J.  
 ; APPLICANT: Vicari, Alain P.  
 ; APPLICANT: Zlotnik, Albert  
 ; TITLE OF INVENTION: Methods for using chemokine TECK  
 ; FILE REFERENCE: DX0589K1D US  
 ; CURRENT APPLICATION NUMBER: US/10759,860  
 ; CURRENT FILING DATE: 2004-01-16  
 ; PRIOR APPLICATION NUMBER: US 10/039,659  
 ; PRIOR FILING DATE: 2002-01-03  
 ; PRIOR APPLICATION NUMBER: US 08/887,977  
 ; PRIOR FILING DATE: 1997-07-03  
 ; PRIOR APPLICATION NUMBER: US 60/021,664  
 ; PRIOR FILING DATE: 1996-07-05  
 ; PRIOR APPLICATION NUMBER: US 60/028,329  
 ; PRIOR FILING DATE: 1996-10-11  
 ; PRIOR APPLICATION NUMBER: US 60/048,593  
 ; PRIOR FILING DATE: 1997-06-04  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 14  
 ; LENGTH: 374  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-759-860-14  
 Query Match 100.0%; Score 1970; DB 17; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-163;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFFGVGN 60  
 Db 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFFGVGN 60  
 Qy 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 Db 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 Qy 121 HIGVFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 Db 121 HIGVFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 Qy 181 CQKEDSVYVCGPYPRGWNPHFTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240  
 Db 181 CQKEDSVYVCGPYPRGWNPHFTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240  
 Qy 241 AVRVIPTIMIVYFLWTPYNIIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 Db 241 AVRVIPTIMIVYFLWTPYNIIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 Qy 301 NPITYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLDGRGKSKI 360  
 Db 301 NPITYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLDGRGKSKI 360  
 Qy 361 GRAPEASLQDKEGA 374  
 Db 361 GRAPEASLQDKEGA 374  
 RESULT 9  
 US-10-799-736-13  
 ; Sequence 13, Application US/10799736  
 ; Publication No. US20050118675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OWMAN, CHRISTER  
 ; TITLE OF INVENTION: HEPTAHMELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4  
 ; TITLE OF INVENTION: RECEPTOR  
 ; FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING  
 ; CURRENT APPLICATION NUMBER: US/10799,736  
 ; PRIOR FILING DATE: 2004-03-15  
 ; PRIOR APPLICATION NUMBER: US/09/893,512  
 ; PRIOR FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: 60/061,789  
 ; PRIOR FILING DATE: 1997-10-14  
 ; PRIOR APPLICATION NUMBER: 60/081,958  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 09/170,069  
 ; PRIOR FILING DATE: 1998-10-13  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 13  
 ; LENGTH: 374  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-799-736-13  
 Query Match 100.0%; Score 1970; DB 17; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-163;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFFGVGN 60  
 Db 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFFGVGN 60  
 Qy 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 Db 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 Qy 121 HIGVFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 Db 121 HIGVFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 Qy 181 CQKEDSVYVCGPYPRGWNPHFTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240  
 Db 181 CQKEDSVYVCGPYPRGWNPHFTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240  
 Qy 241 AVRVIPTIMIVYFLWTPYNIIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 Db 241 AVRVIPTIMIVYFLWTPYNIIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 Qy 301 NPITYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLDGRGKSKI 360  
 Db 301 NPITYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLDGRGKSKI 360  
 Qy 361 GRAPEASLQDKEGA 374  
 Db 361 GRAPEASLQDKEGA 374  
 RESULT 10  
 US-09-779-879A-9  
 ; Sequence 9, Application US/09779879A  
 ; Patent No. US20020048786A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen, Craig A.  
 ; APPLICANT: Roehke, Viktor  
 ; APPLICANT: Li, Yi  
 ; APPLICANT: Ruben, Steven, M.  
 ; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

Db 361 GRAPEASLQDKEGA 374  
 RESULT 9  
 US-10-799-736-13  
 ; Sequence 13, Application US/10799736  
 ; Publication No. US20050118675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OWMAN, CHRISTER  
 ; TITLE OF INVENTION: HEPTAHMELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4  
 ; TITLE OF INVENTION: RECEPTOR  
 ; FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING  
 ; CURRENT APPLICATION NUMBER: US/10799,736  
 ; PRIOR FILING DATE: 2004-03-15  
 ; PRIOR APPLICATION NUMBER: US/09/893,512  
 ; PRIOR FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: 60/061,789  
 ; PRIOR FILING DATE: 1997-10-14  
 ; PRIOR APPLICATION NUMBER: 60/081,958  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 09/170,069  
 ; PRIOR FILING DATE: 1998-10-13  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 13  
 ; LENGTH: 374  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-799-736-13  
 Query Match 100.0%; Score 1970; DB 17; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-163;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFFGVGN 60  
 Db 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFFGVGN 60  
 Qy 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 Db 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 Qy 121 HIGVFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 Db 121 HIGVFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 Qy 181 CQKEDSVYVCGPYPRGWNPHFTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240  
 Db 181 CQKEDSVYVCGPYPRGWNPHFTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240  
 Qy 241 AVRVIPTIMIVYFLWTPYNIIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 Db 241 AVRVIPTIMIVYFLWTPYNIIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 Qy 301 NPITYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLDGRGKSKI 360  
 Db 301 NPITYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLDGRGKSKI 360  
 Qy 361 GRAPEASLQDKEGA 374  
 Db 361 GRAPEASLQDKEGA 374  
 RESULT 10  
 US-09-779-879A-9  
 ; Sequence 9, Application US/09779879A  
 ; Patent No. US20020048786A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen, Craig A.  
 ; APPLICANT: Roehke, Viktor  
 ; APPLICANT: Li, Yi  
 ; APPLICANT: Ruben, Steven, M.  
 ; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

FILE REFERENCE: 1488.115000A  
; CURRENT APPLICATION NUMBER: US/09/779,879A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 9  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-879A-9

Query Match 92.5%; Score 1823; DB 9; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2e-150;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EVVTFDDYDYGAPCHKFDVKQIQAQLLPPLYSLVFIKFGVGNMLVVLILINCKKLCLT 77  
Db 1 EVVTFDDYDYGAPCHKFDVKQIQAQLLPPLYSLVFIKFGVGNMLVVLILINCKKLCLT 60

QY 78 DIYLLNLAISSDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGVFGGIFFIILLTID 137  
Db 61 DIYLLNLAISSDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGVFGGIFFIILLTID 120

QY 138 RYLAIHVAHFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 197  
Db 121 RYLAIHVAHFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 180

QY 198 WNNFHTIMRNILGLVPLLIIMVICYSGILKTLRCKNEKRRHRAVRVIFTIMIVYFLFWT 257  
Db 181 WNNFHTIMRNILGLVPLLIIMVICYSGILKTLRCKNEKRRHRAVRVIFTIMIVYFLFWT 240

QY 258 PYNIVILLNTFQFFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLPH 317  
Db 241 PYNIVILLNTFQFFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLPH 300

QY 318 IALGCRIPALQKPEVCGPGVPRGKNNKVVTTQGLLDGRGKKSIG 361  
Db 301 IALGCRIPALQKPEVCGPGVPRGKNNKVVTTQGLLDGRGKKSIG 344

RESULT 11  
US-09-779-880A-9  
; Sequence 9, Application US/09779880A  
; Patent No. US20020061834A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10  
; FILE REFERENCE: 1488.115000C  
; CURRENT APPLICATION NUMBER: US/09/779,880A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 9  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-880A-9

Query Match 92.5%; Score 1823; DB 9; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2e-150;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EVVTFDDYDYGAPCHKFDVKQIQAQLLPPLYSLVFIKFGVGNMLVVLILINCKKLCLT 77  
Db 1 EVVTFDDYDYGAPCHKFDVKQIQAQLLPPLYSLVFIKFGVGNMLVVLILINCKKLCLT 60

QY 78 DIYLLNLAISSDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGVFGGIFFIILLTID 137  
Db 61 DIYLLNLAISSDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGVFGGIFFIILLTID 120

QY 138 RYLAIHVAHFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 197  
Db 121 RYLAIHVAHFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 180

QY 198 WNNFHTIMRNILGLVPLLIIMVICYSGILKTLRCKNEKRRHRAVRVIFTIMIVYFLFWT 257  
Db 181 WNNFHTIMRNILGLVPLLIIMVICYSGILKTLRCKNEKRRHRAVRVIFTIMIVYFLFWT 240

QY 258 PYNIVILLNTFQFFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLPH 317  
Db 241 PYNIVILLNTFQFFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLPH 300

QY 318 IALGCRIPALQKPEVCGPGVPRGKNNKVVTTQGLLDGRGKKSIG 361  
Db 301 IALGCRIPALQKPEVCGPGVPRGKNNKVVTTQGLLDGRGKKSIG 344

RESULT 12  
US-10-232-686-9  
; Sequence 9, Application US/10232686  
; Publication No. US20030023044A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCRS) HDGNR10  
; FILE REFERENCE: 1488.115000N  
; CURRENT APPLICATION NUMBER: US/10/232,686  
; CURRENT FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: 09/339,912  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 09/195,662  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 08/466,343  
; PRIOR FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 9  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-232-686-9

Query Match 92.5%; Score 1823; DB 14; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2e-150;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EVVTFDDYDYGAPCHKFDVKQIQAQLLPPLYSLVFIKFGVGNMLVVLILINCKKLCLT 77  
Db 1 EVVTFDDYDYGAPCHKFDVKQIQAQLLPPLYSLVFIKFGVGNMLVVLILINCKKLCLT 60

QY 78 DIYLLNLAISSDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGVFGGIFFIILLTID 137  
Db 61 DIYLLNLAISSDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGVFGGIFFIILLTID 120

QY 138 RYLAIHVAHFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 197  
Db 121 RYLAIHVAHFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 180

QY 198 WNNFHTIMRNILGLVPLLIIMVICYSGILKTLRCKNEKRRHRAVRVIFTIMIVYFLFWT 257  
Db 181 WNNFHTIMRNILGLVPLLIIMVICYSGILKTLRCKNEKRRHRAVRVIFTIMIVYFLFWT 240



Qy 258 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 317  
 Db 241 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 300  
 Qy 318 IALGCRITAPLQKPCVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 361  
 Db 301 IALGCRITAPLQKPCVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 344

RESULT 13

US-10-067-800-9  
 ; Sequence 9, Application US/10067800  
 ; Publication No. US20030100058A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen, Craig A.  
 ; APPLICANT: Roschke, Viktor  
 ; APPLICANT: Ruben, Steven, M.  
 ; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10  
 ; FILE REFERENCE: 1488.1150001  
 ; CURRENT FILING DATE: 2002-02-08  
 ; PRIOR APPLICATION NUMBER: PCT/US01/04153  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 09/779,880  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/297,257  
 ; PRIOR FILING DATE: 2001-06-12  
 ; PRIOR APPLICATION NUMBER: 60/310,458  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: 60/328,447  
 ; PRIOR FILING DATE: 2001-10-12  
 ; PRIOR APPLICATION NUMBER: 60/341,725  
 ; PRIOR FILING DATE: 2001-12-21  
 ; NUMBER OF SEQ ID NOS: 70  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 9  
 ; LENGTH: 344  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-067-800-9

Query Match 92.5%; Score 1823; DB 14; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2e-150;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 BEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIFGVGNMVLVILINCKKLCLT 77  
 Db 1 BEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIFGVGNMVLVILINCKKLCLT 60

Qy 78 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137  
 Db 61 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy 138 RYLAIVHAVFALKARTVTFGVTTSVITLWVAVFASVPGIIFTKCKEDSVVVCPPYPRG 197  
 Db 121 RYLAIVHAVFALKARTVTFGVTTSVITLWVAVFASVPGIIFTKCKEDSVVVCPPYPRG 180

Qy 198 WNNPHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIFTIMIVYFLFWT 257  
 Db 181 WNNPHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIFTIMIVYFLFWT 240

Qy 258 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 317  
 Db 241 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 300

Qy 318 IALGCRITAPLQKPCVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 361  
 Db 301 IALGCRITAPLQKPCVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 344

RESULT 14

US-10-135-839-9

; Sequence 9, Application US/10135839  
 ; Publication No. US20030166024A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen, Craig A.  
 ; APPLICANT: Roschke, Viktor  
 ; APPLICANT: Li, Yi  
 ; APPLICANT: Ruben, Steven, M.  
 ; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10  
 ; FILE REFERENCE: 1488.115000A  
 ; CURRENT APPLICATION NUMBER: US/10/135,839  
 ; CURRENT FILING DATE: 2002-05-01  
 ; PRIOR APPLICATION NUMBER: US/09/779,879A  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: US 60/187,999  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: US 60/234,336  
 ; PRIOR FILING DATE: 2000-09-22  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 344  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-135-839-9

Query Match 92.5%; Score 1823; DB 14; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 2e-150;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 BEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIFGVGNMVLVILINCKKLCLT 77  
 Db 1 BEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIFGVGNMVLVILINCKKLCLT 60

Qy 78 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137  
 Db 61 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy 138 RYLAIVHAVFALKARTVTFGVTTSVITLWVAVFASVPGIIFTKCKEDSVVVCPPYPRG 197  
 Db 121 RYLAIVHAVFALKARTVTFGVTTSVITLWVAVFASVPGIIFTKCKEDSVVVCPPYPRG 180

Qy 198 WNNPHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIFTIMIVYFLFWT 257  
 Db 181 WNNPHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIFTIMIVYFLFWT 240

Qy 258 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 317  
 Db 241 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 300

Qy 318 IALGCRITAPLQKPCVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 361  
 Db 301 IALGCRITAPLQKPCVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 344

RESULT 15

US-09-725-285-9  
 ; Sequence 9, Application US/09725285  
 ; Patent No. US20010000241A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Yi  
 ; APPLICANT: Ruben, Steven, M.  
 ; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10  
 ; FILE REFERENCE: 1488.1150003  
 ; CURRENT APPLICATION NUMBER: US/09/725,285  
 ; CURRENT FILING DATE: 2000-11-29  
 ; PRIOR APPLICATION NUMBER: 09/339,912  
 ; PRIOR FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: 09/195,662  
 ; PRIOR FILING DATE: 1998-11-18  
 ; PRIOR APPLICATION NUMBER: 08/466,343  
 ; PRIOR FILING DATE: 1995-06-06  
 ; NUMBER OF SEQ ID NOS: 9

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-725-285-9

Query Match      87.7%; Score 1727.5; DB 9; Length 329;
Best Local Similarity 95.6%; Pred. No. 4e-142;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 18 EEVTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLSVFIFFGVGNMLVVLIIINCKKXCLT 77
Db 1 EEVTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLSVFIFFGVGNMLVVLIIINCKKXCLT 60

QY 78 DIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
Db 61 DIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

QY 138 RYLAIHVHAEFALKARTVTFGVTSVITLWAVFASVPGIIFTCKOKEDSVVCGPYFPRG 197
Db 106 RYLAIHVHAEFALKARTVTFGVTSVITLWAVFASVPGIIFTCKOKEDSVVCGPYFPRG 165

QY 198 WNNFHTIMRNILGLVPLLIWVICYSGILKTLRCRNEKRRHRAVRVIFTIMIVYFLEWT 257
Db 166 WNNFHTIMRNILGLVPLLIWVICYSGILKTLRCRNEKRRHRAVRVIFTIMIVYFLEWT 225

QY 258 PYNIVILLNTFQBFGLSNCESTSOLDQAQTQTETLGMTHCCINPIIYAFVGEKFRSLFH 317
Db 226 PYNIVILLNTFQBFGLSNCESTSOLDQAQTQTETLGMTHCCINPIIYAFVGEKFRSLFH 285

QY 318 IALGCRITAPLQKPVCGGPGVPRGKNVKTQTQGLLDGRGKSG 361
Db 286 IALGCRITAPLQKPVCGGPGVPRGKNVKTQTQGLLDGRGKSG 329
```

Search completed: June 9, 2005, 17:06:37  
Job time : 106.455 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:27:48 ; Search time 111.826 Seconds  
(without alignments)  
1245.097 Million cell updates/sec

Title: US-10-791-166-4

Perfect score: 1900

Sequence: 1 MLSTSRFRIRNTNBSGEV.....DGVSTNTPTSGQEVSAAGL 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1900	100.0	360	2 AAR79166	Aar79166 Human mon
2	1900	100.0	360	2 AAW35833	Aaw35833 Human mon
3	1900	100.0	360	4 AAG80108	Aag80108 Human CCR
4	1900	100.0	360	4 AAU07614	Aau07614 Human wil
5	1900	100.0	360	6 ABP97725	Abp97725 Amino aci
6	1900	100.0	360	6 ABP81987	Abp81987 Human C-C
7	1900	100.0	360	8 ADM67225	Adm67225 Human adi
8	1900	100.0	360	8 ADL82831	Adl82831 Human PRO
9	1899	99.9	360	4 AAU07613	Aau07613 Human CCR
10	1894	99.7	360	4 ABB56340	Abb56340 Non-endog
11	1838	96.7	347	7 ADF56627	Adf56627 Partial h
12	1651.5	86.9	374	2 AAR79165	Aar79165 Human mon
13	1651.5	86.9	374	4 AAG80107	Aag80107 Human CCR
14	1651.5	86.9	374	6 ABU09083	Abu09083 Human che
15	1651.5	86.9	374	7 ADD44861	Add44861 Human PRO
16	1651.5	86.9	374	7 ADD44865	Add44865 Human PRO
17	1651.5	86.9	374	7 ADP65146	Adp65146 Human che
18	1651.5	86.9	374	8 ADO29221	Ado29221 Human GPC
19	1651.5	86.9	374	8 ADQ67847	Adq67847 Human che
20	1568.5	82.6	344	5 ABG92881	Abg92881 Class I r
21	1568.5	82.6	344	6 ABU61655	Abu61655 Human mon
22	1568.5	82.6	344	7 ADP72129	Adp72129 Human G-p
23	1568.5	82.6	344	7 ADP86217	Adp86217 Human MCP
24	1535	80.8	373	8 ADM67224	Adm67224 Murine ad
25	1535	80.8	373	8 ADO29222	Ado29222 Mouse GPC

26	1535	80.8	373	8 ADP74040	Adp74040 Murine CC
27	1473	77.5	329	4 AAB46859	Aab46859 Human MCP
28	1473	77.5	329	5 ABB81055	Abb81055 Human MCP
29	1473	77.5	329	8 ADR16266	Adr16266 Human MCP
30	1396	73.5	354	8 ADO29228	Ado29228 Mouse GPC
31	1386	72.9	354	2 AAW54037	Aaw54037 Mouse CC-
32	1386	72.9	354	7 ADD44859	Add44859 Rat Prote
33	1386	72.9	354	7 ADD44863	Add44863 Rat Prote
34	1371	72.2	352	4 AAG79089	Aag79089 Amino aci
35	1364	71.8	352	2 AAW27407	Aaw27407 Human CCR
36	1364	71.8	352	2 AAW27123	Aaw27123 Human che
37	1364	71.8	352	2 AAW27125	Aaw27125 Macaque c
38	1364	71.8	352	2 AAW23835	Aaw23835 Human CC
39	1364	71.8	352	2 AAW88232	Aaw88232 HIV-1 co-
40	1364	71.8	352	4 AAG80111	Aag80111 Human CCR
41	1364	71.8	352	4 AAE04321	Aae04321 Human che
42	1364	71.8	352	4 AAB83354	Aab83354 Human CCR
43	1364	71.8	352	4 AAB82948	Aab82948 Human HIV
44	1364	71.8	352	5 AAM52828	Aam52828 Human CC
45	1364	71.8	352	5 ABB08343	Abb08343 Human che

ALIGNMENTS

RESULT 1  
AAR79166  
ID AAR79166 standard; protein; 360 AA.  
XX  
AC AAR79166;  
XX  
DT 25-MAR-2003 (revised)  
DT 29-DEC-1995 (first entry)  
XX  
XX Human monocyte chemoattractant protein-1 receptor MCP-1RB.  
DE Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Domain 1..48  
FT /label= extracellular  
FT Domain 49..70  
FT /label= transmembrane  
FT Domain 80..700  
FT /label= transmembrane  
FT Domain 115..136  
FT /label= transmembrane  
FT Domain 154..178  
FT /label= transmembrane  
FT Domain 204..231  
FT /label= transmembrane  
FT Domain 244..268  
FT /label= transmembrane  
FT Domain 295..313  
FT /label= transmembrane  
FT Region 314..360  
FT /label= carboxyl tail  
XX  
XX WO9519436-A1.  
XX  
XX 20-JUL-1995.  
XX  
XX 11-JAN-1995; 95WO-US0000476.  
XX  
XX 13-JAN-1994; 94US-00182962.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Charo I, Coughlin S;  
XX  
XX WPI; 1995-263866/34.  
DR

DR N-PSDB; AAQ96298.  
 XX DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.  
 PT for identifying antagonists and for treating diseases characterised by  
 PT monocyte infiltrates.  
 XX  
 PS Claim 2; Fig 2; 84pp; English.  
 XX  
 CC To identify and clone new members of the chemokine receptor gene family,  
 CC degenerate oligo primers were designed corresp. to the conserved  
 CC sequences R79167 in the second and R79168 in the third transmembrane  
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the  
 CC HUMSTRS orphan receptor (GenBank Accession #M99293). The degenerate oligo  
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and  
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers  
 CC yielded a number of PCR products. One cDNA appeared to encode a novel  
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA  
 CC library was constructed in pROG and probed with the PCR product. A 2.1  
 CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA  
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA  
 CC sequence first obtd. from the 5' UTR through the putative seventh  
 CC transmembrane domain but contained a different cytoplasmic tail. The  
 CC second sequence appears to represent alternative splicing of the carboxyl  
 CC C-terminal tail of the MCP-1R protein. The two sequences are denoted MCP-  
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-  
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.  
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct FN  
 CC field.)  
 XX  
 SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 2; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-206;  
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRSRFRINTNESGEEVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVN 60  
 DB 1 MLSTSRSRFRINTNESGEEVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVN 60  
 QY 61 MLVVLLINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 DB 61 MLVVLLINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 QY 121 HIGYFGGIFPIILLTIDRYLAIHVAVFALKARTVTGVTSVITWLVAVPASVPGIIFTK 180  
 DB 121 HIGYFGGIFPIILLTIDRYLAIHVAVFALKARTVTGVTSVITWLVAVPASVPGIIFTK 180  
 QY 181 CQKEDSVYVCGPYPPFGNNFHTIMRNILGLVPLLIWVICYSGLKTLRLCRNEKKRHR 240  
 DB 181 CQKEDSVYVCGPYPPFGNNFHTIMRNILGLVPLLIWVICYSGLKTLRLCRNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
 DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFRRLYSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360  
 DB 301 NPIIYAFVGEKFRRLYSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360

RESULT 2  
 AAW35833  
 ID AAW35833 standard; protein; 360 AA.  
 AC  
 AC AAW35833;  
 XX  
 XX 27-FEB-1998 (first entry)

XX Human monocyte chemoattractant protein 1 receptor.  
 DE  
 XX Human; MCP-1; monocyte chemoattractant protein; receptor; tumour;  
 XX inflammatory disease; viral; allergy; diabetes.  
 XX

OS Homo sapiens.  
 XX  
 PN JF09238688-A.  
 XX  
 PD 16-SEP-1997.  
 XX  
 PF 11-MAR-1996; 96JP-00053574.  
 XX  
 PR 11-MAR-1996; 96JP-00053574.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 DR WPI; 1997-506557/47.  
 DR N-PSDB; AAT96976.  
 XX  
 PT DNA encoding human monocyte chemoattractant protein 1 receptor - used to  
 PT treat tumours and inflammatory, viral, infectious, allergic, diabetic and  
 PT central nervous system diseases.  
 PS Disclosure; Page 12-14; 15pp; Japanese.  
 XX  
 CC The present sequence represents human monocyte chemoattractant protein 1  
 CC (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA are  
 CC used for the prevention and treatment of tumours and inflammatory, viral,  
 CC infectious, allergic, diabetic and central nervous system diseases  
 XX  
 SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 2; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-206;  
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLSTSRSRFRINTNESGEEVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVN 60  
 DB 1 MLSTSRSRFRINTNESGEEVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVN 60  
 QY 61 MLVVLLINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 DB 61 MLVVLLINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120  
 QY 121 HIGYFGGIFPIILLTIDRYLAIHVAVFALKARTVTGVTSVITWLVAVPASVPGIIFTK 180  
 DB 121 HIGYFGGIFPIILLTIDRYLAIHVAVFALKARTVTGVTSVITWLVAVPASVPGIIFTK 180  
 QY 181 CQKEDSVYVCGPYPPFGNNFHTIMRNILGLVPLLIWVICYSGLKTLRLCRNEKKRHR 240  
 DB 181 CQKEDSVYVCGPYPPFGNNFHTIMRNILGLVPLLIWVICYSGLKTLRLCRNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
 DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFRRLYSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360  
 DB 301 NPIIYAFVGEKFRRLYSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360

RESULT 3  
 AAG80108  
 ID AAG80108 standard; protein; 360 AA.  
 AC  
 AC AAG80108;  
 XX  
 XX 17-JAN-2002 (first entry)

XX Human CCR2b protein.  
 XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
 XX inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
 XX chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
 XX antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
 XX antirheumatic; antiarthritic.  
 XX

OS	Homo sapiens.
XX	
PN	WO200172830-A2.
XX	
PD	04-OCT-2001.
XX	
PF	02-APR-2001; 2001WO-EP003708.
XX	
PR	31-MAR-2000; 2000DE-01016013.
XX	
PA	(IPFP-) IPF PHARM GMBH.
PA	(FORS/) FORSSMANN U.
XX	
PI	Forsmann W, Adermann K, Heitland A, Spodsborg N;
XX	
DR	WPI; 2001-626256/72.
XX	
PT	Diagnostic agent containing two or more receptor-specific ligands, useful
PT	for detecting tumors, inflammation etc., also therapeutic use of ligand
PT	inhibitors.
XX	
PS	Disclosure; Page 9; 26pp; German.
XX	
CC	This invention describes a novel diagnostic agent (A) comprising at least
CC	two different ligands (I) for receptors (II) that are implicated in
CC	disease. (A) are used for the diagnosis of tumors (especially colorectal
CC	or prostatic), organ rejection, inflammation and autoimmune diseases.
CC	Also inhibitors of (I) are used therapeutically against tumors (and their
CC	metastases), inflammation (particularly bronchial asthma or chronic bowel
CC	inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC	where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC	endocrine, motor or urogenital systems or skin are affected, and bone
CC	marrow diseases. The products of the invention are chemokine derivatives
CC	which have cytostatic, antiinflammatory, antiaesthetic,
CC	immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC	Chemokines act on specific tumor and inflammatory cells through a
CC	constellation of chemokine receptors (CR), which control migration and
CC	proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC	fragments used to illustrate the method of the invention
XX	
SQ	Sequence 360 AA;
Query Match            100.0%; Score 1900; DB 4; Length 360;	
Best Local Similarity    100.0%; Pred. No. 1.9e-206;	
Matches 360; Conservative    0; Mismatches    0; Indels    0; Gaps    0;	
Qy	1 MLSTSRGRFRINTNESGEVTTFFDDYDGAPCHKFDVKQIGAOQLLPPLYSLVTFPGFVGN 60
Db	1 MLSTSRGRFRINTNESGEVTTFFDDYDGAPCHKFDVKQIGAOQLLPPLYSLVTFPGFVGN 60
Qy	61 MLVVLLINCKKACLTIDYLNLAIISDLLFLITLPLWAHSAAENEWFGNAWKLFGLY 120
Db	61 MLVVLLINCKKACLTIDYLNLAIISDLLFLITLPLWAHSAAENEWFGNAWKLFGLY 120
Qy	121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVTVTSITWLVAVFASVPGIIFTK 180
Db	121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVTVTSITWLVAVFASVPGIIFTK 180
Qy	181 CQKEDSVVCGPYPPRGNNPHFTMRNLTGLVLPLLIMVICYGILKTLLRCNEKKRRH 240
Db	181 CQKEDSVVCGPYPPRGNNPHFTMRNLTGLVLPLLIMVICYGILKTLLRCNEKKRRH 240
Qy	241 AVRVIPTMIIVYFLFWTPYNYVILLNTFOEPPGFSNCBSTSQLODQATQVETLGMTHCCI 300
Db	241 AVRVIPTMIIVYFLFWTPYNYVILLNTFOEPPGFSNCBSTSQLODQATQVETLGMTHCCI 300
Qy	301 NPITIYAFGEKFRYLSVFFRKHTIKRCKCPFYRETVDGVSTNTPTSGEOEVSAGL 360
Db	301 NPITIYAFGEKFRYLSVFFRKHTIKRCKCPFYRETVDGVSTNTPTSGEOEVSAGL 360
RESULT 4	
AU07614	

ID	AAU07614 standard; protein; 360 AA.	
XX		
AC	AAU07614;	
XX		
DT	04-DEC-2001 (first entry)	
XX		
DE	Human wild-type CCR2-64V polypeptide.	
XX		
KW	Human; CCR2 receptor; CCR2-641; CCR2-64V; gene therapy; atherosclerosis;	
KW	single nucleotide polymorphism; hypercholesterolaemia.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200162796-A1.	
XX		
PD	30-AUG-2001.	
XX		
PF	22-FEB-2001; 2001WO-GB000755.	
XX		
PR	22-FEB-2000; 2000GB-00004183.	
XX		
PA	(SMIK ) SMITHKLINE BEECHAM PLC.	
XX		
PI	Valdes AM, Groot PHE, Spurr NK;	
XX		
DR	WPI; 2001-550086/61.	
DR	N-PSDB; AAS12140.	
XX		
CC	Diagnosing atherosclerosis or susceptibility to atherosclerosis in a	
PT	subject, by determining a single nucleotide polymorphism in specific	
PT	codon of a polynucleotide encoding human CCR2 receptor in genome of the	
PT	subject.	
XX		
PS	Claim 1; Page 21; 28pp; English.	
XX		
CC	The invention relates to diagnosing atherosclerosis (or susceptibility	
CC	to) in a subject by determining expression or activity of the human CCR2-	
CC	641 polypeptide (a polymorphic variant form of the human CCR2 receptor)	
CC	or the CCR2-64V polypeptide (human CCR2 receptor), by screening for a	
CC	single nucleotide polymorphism in codon 64 of the polynucleotide encoding	
CC	the CCR2 receptor. This results in production of CCR2-641, whereby	
CC	polymorphic variants are associated with a lower incidence of	
CC	atherosclerosis. The presence or amount of CCR2-641/V in a sample can	
CC	also be analysed. The sequences of the invention can be used for	
CC	predicting the response of a patient to drug treatment, for predicting	
CC	the disease outcome in a patient and also for the production of a	
CC	treatment for hypercholesterolaemia. The sequence represents the wild-	
CC	type receptor polypeptide CCR2-64V	
XX		
SQ	Sequence 360 AA;	
	Query Match 100.0%; Score 1900; DB 4; Length 360;	
	Best Local Similarity 100.0%; Pred. No. 1.9e-206;	
	Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	1 MLSTSRFRIRNTNESGEVTFPDYDGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60	
Db	1 MLSTSRFRIRNTNESGEVTFPDYDGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60	
Qy	61 MLVVLILINCKLCLTDIYLLNLAISDLLFLITPLWAHSAANEWFGNAMCKLFTGLY 120	
Db	61 MLVVLILINCKLCLTDIYLLNLAISDLLFLITPLWAHSAANEWFGNAMCKLFTGLY 120	
Qy	121 HIGYFGGIFPIILLTIDRYLAIAVHAFALKARTVTFGVTSVITWLVAFVASVPGIITK 180	
Db	121 HIGYFGGIFPIILLTIDRYLAIAVHAFALKARTVTFGVTSVITWLVAFVASVPGIITK 180	
Qy	181 CQKEDSVYVCGPFFPRGNNFHTIMRNILGVLPULLIMVICYSGILKTLRCRNEKKRHR 240	
Db	181 CQKEDSVYVCGPFFPRGNNFHTIMRNILGVLPULLIMVICYSGILKTLRCRNEKKRHR 240	
Qy	241 AVRVIPTIMTVFLFWTPYNNIVILLNTFQBFPLGNSCESTSOLDQATQVETLGMTHCCI 300	

Db 241 AVRVIPTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSLDQATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPSTGQEVSA 360  
 Db 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPSTGQEVSA 360  
 RESULT 5  
 ABP97725  
 ID ABP97725 standard; protein; 360 AA.  
 XX AC ABP97725;  
 XX  
 XX 28-MAY-2003 (first entry)  
 XX  
 DE Amino acid sequence of human chemokine receptor CCR2.  
 XX  
 KW Human; chemokine receptor; CCR2; viral infection; surface protein;  
 KW respiratory virus infection; respiratory syncytial virus infection;  
 KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003014153-A2.  
 PN  
 XX  
 PD 20-FEB-2003.  
 XX  
 XX 12-AUG-2002; 2002WO-CA001248.  
 PF  
 XX  
 PR 10-AUG-2001; 2001US-0311088P.  
 XX  
 XX (TOPI-) TOPIGEN PHARM INC.  
 PA  
 XX Renzi P, Zemzoui K;  
 PI  
 XX WPI; 2003-256541/25.  
 DR N-PSDB; ABZ68878.  
 DR  
 XX  
 XX Modulating viral infection of a cell, for treating or preventing  
 PT respiratory virus infections, bronchitis, pneumonia or asthma, by  
 PT modulating a binding interaction between a cell chemokine-receptor and a  
 PT surface protein of the virus.  
 XX  
 XX Disclosure; Page 82-84; 120pp; English.  
 PS  
 XX  
 XX The present sequence represents human chemokine receptor CCR2. The  
 CC specification describes a method for modulating viral infection of a  
 CC cell. the method comprises modulating a binding interaction between a  
 CC cell chemokine-receptor and a surface protein of the virus. The proviso  
 CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is  
 CC not HIV. The method is useful for treating or preventing respiratory  
 CC virus infection in vertebrates, more particularly respiratory syncytial  
 CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,  
 CC bronchitis, pneumonia or asthma  
 XX  
 SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 6; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-206;  
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRSRFRNTNNEGSEVTFPDYDYGAPCHKFDVKQIGALLPPLYSLVIFGFGVN 60  
 Db 1 MLSTSRSRFRNTNNEGSEVTFPDYDYGAPCHKFDVKQIGALLPPLYSLVIFGFGVN 60  
 QY 61 MLVVLLINCKKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
 Db 61 MLVVLLINCKKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
 QY 121 HGVFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVWTSVITLWVAFASVPGIIFTK 180  
 Db 121 HGVFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVWTSVITLWVAFASVPGIIFTK 180

QY 181 CQKEDSVYVCGPYFPRGWNNEFTIMRNILGLVPLLIWVICYSILKTLRCNEKRRH 240  
 Db 181 CQKEDSVYVCGPYFPRGWNNEFTIMRNILGLVPLLIWVICYSILKTLRCNEKRRH 240  
 QY 241 AVRVIPTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSLDQATQVTTGLMTHCCI 300  
 Db 241 AVRVIPTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSLDQATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPSTGQEVSA 360  
 Db 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPSTGQEVSA 360  
 RESULT 6  
 ABP81987  
 ID ABP81987 standard; protein; 360 AA.  
 XX AC ABP81987;  
 XX  
 XX 04-MAR-2003 (first entry)  
 XX  
 XX Human C-C chemokine receptor 2 protein SEQ ID NO:460.  
 DE  
 XX  
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200261087-A2.  
 PN  
 XX  
 PD 08-AUG-2002.  
 XX  
 XX 19-DEC-2001; 2001WO-US050107.  
 PF  
 XX  
 XX 19-DEC-2000; 2000US-0257144P.  
 PR  
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
 PA  
 XX Burmer GC, Roush CL, Brown JP;  
 PI  
 XX WPI; 2003-046718/04.  
 DR N-PSDB; ABZ42835.  
 DR  
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 PT  
 XX Disclosure; Fig 1; 523pp; English.  
 PS  
 XX The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (i) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,

CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunosays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 6; Length 360;  
Best Local Similarity 100.0%; Pred. No. 1.9e-206;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGALLPPLYSILVIFGVGN 60  
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGALLPPLYSILVIFGVGN 60  
QY 61 MLVVLILINCKKLCITDIYLLNLAI SDLLFLITPLWAHSAANEVFGNAMCKLFTGLY 120  
DB 61 MLVVLILINCKKLCITDIYLLNLAI SDLLFLITPLWAHSAANEVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIPFIILLTIDRYLAIVHAFKARTVTGVTSTVITLWVAFASVPGIIFTK 180  
DB 121 HIGYFGGIPFIILLTIDRYLAIVHAFKARTVTGVTSTVITLWVAFASVPGIIFTK 180  
QY 181 COKEDSVYVCGPYPRGWNFNHIMNIGLVPLLMVICYSGILKTLRCNEKKRHR 240  
DB 181 COKEDSVYVCGPYPRGWNFNHIMNIGLVPLLMVICYSGILKTLRCNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLWTPYNNIVLLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
DB 241 AVRVIPTIMIVYFLWTPYNNIVLLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFFPRKHITKRCQCPVYRETVDGVTSTNTPSTGEQVSAGL 360  
DB 301 NPIIYAFVGEKFRYLSVFFPRKHITKRCQCPVYRETVDGVTSTNTPSTGEQVSAGL 360

RESULT 7  
ADM67225  
ID ADM67225 standard; protein; 360 AA.  
XX  
AC ADM67225;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human adipocyte specific chemokine (C-C) receptor 2 protein SeqID 579.

DE human; adipocyte specific; adipose tissue; anti-obesity;  
XX high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;  
KW adipogenesis; hypertension; cardiovascular disease; anorectic;  
KW antidiabetic; hypotensive; chemokine (C-C) receptor 2.

OS Homo sapiens.

XX WO2004011618-A2.

PN 05-FEB-2004.

XX 29-JUL-2003; 2003WO-US023684.

XX 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

XX (HMGE-) HMGNE INC.

XX Chada K, Chouinard R, Ashar H, Sayed AMD;

XX

DR WPI; 2004-143846/14.  
XX N-PSDB; ADM66946.

XX Identifying adipocyte specific genes, useful for treating obesity or  
PT diabetes, and for identifying drug targets, by differential gene  
PT expression analysis between adipose tissue or stromal vascular tissue of  
PT mice of different genotypes.

XX Disclosure; SEQ ID NO 579; 91pp; English.

XX This invention relates to a novel method for identifying genes that are  
CC over-expressed in adipose tissue and as such it provides targets for anti  
CC -obesity pharmaceutical compositions. Specifically, it refers to a high  
CC mobility group I-C protein (HMGI-C) that is associated with obesity and  
CC is epistatic to leptin, furthermore, it refers to the ob gene where an  
CC autosomal recessive trait is linked to obesity and diabetes. The present  
CC invention describes performing differential gene expression analysis  
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)  
CC of any two different mice selected from a group consisting of wild-type,  
CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using  
CC this method novel nucleotides and the encoded proteins thereof were  
CC identified that are adipocyte specific, and as such can be used for  
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,  
CC hypertension and cardiovascular disease, as well as screening for  
CC compounds that can modulate or prevent adipogenesis and treat diabetes or  
CC obesity. These compositions exhibit anorectic, antidiabetic and  
CC hypotensive activities. This polypeptide sequence is a human homologue of  
CC a murine adipocyte specific protein sequence of the invention.

XX Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 1.9e-206;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGALLPPLYSILVIFGVGN 60  
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGALLPPLYSILVIFGVGN 60  
QY 61 MLVVLILINCKKLCITDIYLLNLAI SDLLFLITPLWAHSAANEVFGNAMCKLFTGLY 120  
DB 61 MLVVLILINCKKLCITDIYLLNLAI SDLLFLITPLWAHSAANEVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIPFIILLTIDRYLAIVHAFKARTVTGVTSTVITLWVAFASVPGIIFTK 180  
DB 121 HIGYFGGIPFIILLTIDRYLAIVHAFKARTVTGVTSTVITLWVAFASVPGIIFTK 180  
QY 181 COKEDSVYVCGPYPRGWNFNHIMNIGLVPLLMVICYSGILKTLRCNEKKRHR 240  
DB 181 COKEDSVYVCGPYPRGWNFNHIMNIGLVPLLMVICYSGILKTLRCNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLWTPYNNIVLLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
DB 241 AVRVIPTIMIVYFLWTPYNNIVLLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFFPRKHITKRCQCPVYRETVDGVTSTNTPSTGEQVSAGL 360  
DB 301 NPIIYAFVGEKFRYLSVFFPRKHITKRCQCPVYRETVDGVTSTNTPSTGEQVSAGL 360

RESULT 8  
ADL82831  
ID ADL82831 standard; protein; 360 AA.

XX AC ADL82831;

XX 17-JUN-2004 (first entry)

XX Human PRO84690, SEQ ID 33.

XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;  
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;  
KW Gene Therapy; PRO; B cell related disorder; cancer;

immune-mediated inflammatory disease; human.  
Homo sapiens.  
WO2004024097-A2.  
25-MAR-2004.  
15-SEP-2003; 2003WO-US029097.  
16-SEP-2002; 2002US-0411392P.  
(GETH ) GENENTECH INC.  
Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI,  
Wu TD;  
WPI; 2004-329389/30.  
N-PSDB; ADL82830.  
New PRO polypeptide, useful for diagnosing and treating a B cell related  
disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune  
mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.  
Claim 10; Fig 33; 695pp; English.  
The present invention relates to PRO proteins and their coding sequences.  
The PRO proteins are useful for diagnosing and treating a B cell related  
disorder, e.g. X-linked infantile hypogammaglobulinemia, polyaccharide  
antigen unresponsiveness, selective IGA deficiency, selective IgM  
deficiency, selective deficiency of IGG subclasses, immunodeficiency with  
hyper IGM, transient hypogammaglobulinemia of infancy, Burkitt's  
lymphoma, intermediate lymphoma, follicular lymphoma, type II  
hyperplasia, rheumatoid arthritis, autoimmune mediated haemolytic  
anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or  
ankylosing spondylitis. The PRO proteins are also useful for preparing a  
medicament for treating a condition that is responsive to the PRO  
protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO  
coding sequences are useful as hybridization probes in chromosome and  
gene mapping, in preparing PRO proteins, or in generating transgenic  
animals or knockout animals, which in turn are useful in the development  
and screening of therapeutically useful reagents.

Sequence 360 AA;  
Query Match 100.0%; Score 1900; DB 8; Length 360;  
Best Local Similarity 100.0%; Pred. No. 1.9e-206;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLSLVIFGFVGN 60  
DB 1 MLSTSRFRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLSLVIFGFVGN 60  
QY 61 MLVLLILINCKKLKCLTDIYLLNLAISSDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
DB 61 MLVLLILINCKKLKCLTDIYLLNLAISSDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAFKARTVTGVTTSVITLWVAVPASVPGIIFTK 180  
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAFKARTVTGVTTSVITLWVAVPASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGNFNHITMRNLGLVPLIMVICYSGILKTLRLCRNEKKRRH 240  
DB 181 CQKEDSVYVCGPYFPRGNFNHITMRNLGLVPLIMVICYSGILKTLRLCRNEKKRRH 240  
QY 241 AVRVIETIMIVYFLFWTPYNYVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
DB 241 AVRVIETIMIVYFLFWTPYNYVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAVGKFRYLSVFRKHTKRCQKCPVFRVRETVDGVTSTNTPSTGQEVSAGL 360  
DB 301 NPIIYAVGKFRYLSVFRKHTKRCQKCPVFRVRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 9  
AAU07613.  
ID AAU07613 standard; protein; 360 AA.  
XX AC AAU07613;  
XX DT 04-DEC-2001 (first entry)  
XX DE Human CCR2-64I polymorphic variant polypeptide.  
XX KW Human; CCR2 receptor; CCR2-64I; CCR2-64V; gene therapy; atherosclerosis;  
XX KW single nucleotide polymorphism; hypercholesterolaemia.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 64 /note= "Wild-type Val is replaced by Ile"  
XX FT  
XX PN WO200162796-A1.  
XX PD 30-AUG-2001.  
XX PF 22-FEB-2001; 2001WO-GB000755.  
XX PR 22-FEB-2000; 2000GB-00004183.  
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX PI Valdes AM, Groot PHE, Spurr NK;  
XX DR WPI; 2001-550086/61.  
XX DR N-PSDB; AAS12139.  
XX PT Diagnosing atherosclerosis or susceptibility to atherosclerosis in a  
XX PT subject, by determining a single nucleotide polymorphism in specific  
XX PT codon of a polynucleotide encoding human CCR2 receptor in genome of the  
XX PT subject.  
XX PS Claim 1; Page 20; 28pp; English.  
XX CC The invention relates to diagnosing atherosclerosis (or susceptibility  
XX CC to) in a subject by determining expression or activity of the human CCR2-  
XX CC 64I polypeptide (a polymorphic variant form of the human CCR2 receptor)  
XX CC or the CCR2-64V polypeptide (human CCR2 receptor), by screening for a  
XX CC single nucleotide polymorphism in codon 64 of the polynucleotide encoding  
XX CC the CCR2 receptor. This results in production of CCR2-64I, whereby  
XX CC polymorphic variants are associated with a lower incidence of  
XX CC atherosclerosis. The presence or amount of CCR2-64I/V in a sample can  
XX CC also be analysed. The sequences or amount of the invention can be used for  
XX CC predicting the response of a patient to drug treatment, for predicting  
XX CC the disease outcome in a patient and also for the production of a  
XX CC treatment for hypercholesterolaemia. The sequence represents the  
XX CC polymorphic variant polypeptide CCR2-64I  
XX SQ Sequence 360 AA;  
Query Match 99.9%; Score 1899; DB 4; Length 360;  
Best Local Similarity 99.7%; Pred. No. 2.4e-206;  
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLSLVIFGFVGN 60  
DB 1 MLSTSRFRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLSLVIFGFVGN 60  
QY 61 MLVLLILINCKKLKCLTDIYLLNLAISSDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
DB 61 MLVLLILINCKKLKCLTDIYLLNLAISSDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAFKARTVTGVTTSVITLWVAVPASVPGIIFTK 180  
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAFKARTVTGVTTSVITLWVAVPASVPGIIFTK 180



QY 181 COKEDSVVCGPYPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCRNEKKRHR 240  
 DB 181 COKEDSVVCGPYPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCRNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQEFGLSNCESTSQLDOATQVTTGLMTHCCI 300  
 DB 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQEFGLSNCESTSQLDOATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360  
 DB 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360

## RESULT 10

ABB56340  
 ID ABB56340 standard; protein; 360 AA.

XX ABB56340;

DT 18-FEB-2002 (first entry)

DE Non-endogenous human GPCR protein, SEQ ID NO: 473.

KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;  
 KW constitutively activated GPCR; agonist; disease.

OS Homo sapiens.

OS Synthetic.

XX WO200177172-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US011098.

XX 07-APR-2000; 2000US-0195747P.

XX (AREN-) ARENA PHARM INC.

XX Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI; 2001-648759/74.

DR N-PSDB; ABI97976.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in  
 PT disease treatment, comprises contacting candidate compounds with versions  
 PT of GPCRs.

XX Claim 1; Page 274-275; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which  
 CC the endogenous ligand has been identified. Non-endogenous constitutively  
 CC activated versions of known GPCRs are used in the invention for the  
 CC direct identification of candidate compounds as receptor agonists,  
 CC inverse agonists or partial agonists. Such agonists are useful as  
 CC therapeutic agents for diseases or disorders associated with GPCRs. The  
 CC present sequence is a non-endogenous version of a known human GPCR

XX Sequence 360 AA;

XX Query Match

XX Best Local Similarity 99.7%; Score 1894; DB 4; Length 360;

XX Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTFDFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVN 60

DB 1 MLSTSRFRIRNTNESGEVTFDFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVN 60

QY 61 MLVLLILINCKKGLCTDIYLLNLAIISDLLLPLTLPWAHSAANEWFGNAMCKLFTGLY 120

DB 61 MLVLLILINCKKGLCTDIYLLNLAIISDLLLPLTLPWAHSAANEWFGNAMCKLFTGLY 120

QY 121 HIGYFGGIFPILLITIDRYLAIVHAVFALKARTTTFGVVTSVITWLVAVFASVPGIIFTK 180  
 DB 121 HIGYFGGIFPILLITIDRYLAIVHAVFALKARTTTFGVVTSVITWLVAVFASVPGIIFTK 180  
 QY 181 COKEDSVVCGPYPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCRNEKKRHR 240  
 DB 181 COKEDSVVCGPYPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCRNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQEFGLSNCESTSQLDOATQVTTGLMTHCCI 300  
 DB 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQEFGLSNCESTSQLDOATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360  
 DB 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360

## RESULT 11

ADF56627

ID ADF56627 standard; protein; 347 AA.

XX ADF56627;

DT 12-FEB-2004 (first entry)

DE Partial human monocyte chemoattractant protein 1 receptor.

KW antiasthmatic; cardiant; hypotensive; antiallergic; neuroprotective;  
 KW osteopathic; vulnary; gene therapy; asthma; acute heart failure;  
 KW hypertension; osteoporosis; allergy; dementia; ulcer; human;  
 KW G protein coupled receptor; HGBER32;  
 KW monocyte chemoattractant protein 1 receptor.

XX Homo sapiens.

XX US2003165901-A1.

XX 04-SEP-2003.

XX 21-JUN-2002; 2002US-00176078.

XX 05-JUN-1995; 95US-00461244.

XX 25-JUN-1998; 98US-00104792.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Soppet DR, Li Y, Rosen CA, Ruben SM;

XX WPI; 2003-898052/82.

XX New polynucleotide, useful for preparing a composition for diagnosing or  
 PT treating e.g. asthma, acute heart failure, hypertension, osteoporosis,  
 PT allergies, dementia or ulcers.

XX Disclosure; SEQ ID NO 3; 28pp; English.

XX The invention describes an isolated polynucleotide comprising a sequence  
 CC encoding the polypeptide comprising a 355 residue amino acid sequence,  
 CC given in the specification, a sequence encoding the polypeptide expressed  
 CC by the DNA contained in ATCC Deposit No. 97187, a sequence that  
 CC hybridises with, or that is at least 70 % identical to them, or a  
 CC sequence fragment of them. The polynucleotide is useful for preparing a  
 CC composition for diagnosing or treating asthma, acute heart failure, a  
 CC hypertension, osteoporosis, allergies, dementia or ulcers. This is the  
 CC amino acid sequence of human monocyte chemoattractant protein 1 receptor  
 CC starting at residue 40 and used in a comparison with human G protein  
 CC coupled receptor HGBER32.

XX Sequence 347 AA;

XX Query Match

XX Best Local Similarity 96.7%; Score 1838; DB 7; Length 347;

XX Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 NESGEEVTFDDYDYGAPCHKFDVKQIGQALLPPLSLVIFGVGNMLVLLINCKKL 73  
 DB 1 NESGEEVTFDDYDYGAPCHKFDVKQIGQALLPPLSLVIFGVGNMLVLLINCKKL 60  
 QY 74 KCLTDIYLLNLAISSDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHICYGFGIPIIL 133  
 DB 61 KCLTDIYLLNLAISSDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHICYGFGIPIIL 120  
 QY 134 LTDRYLAIHVAHFALKARTVTFGVTSVITLWVAVPASVPGIIFTKCKEDSVYVCGPY 193  
 DB 121 LTDRYLAIHVAHFALKARTVTFGVTSVITLWVAVPASVPGIIFTKCKEDSVYVCGPY 180  
 QY 194 FPRGWNFFHIMRNILGLVPLIMVICYSGLKTLRCNEKKRHRVAVIITMIVYF 253  
 DB 181 FPRGWNFFHIMRNILGLVPLIMVICYSGLKTLRCNEKKRHRVAVIITMIVYF 240  
 QY 254 LFWTYPYVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFR 313  
 DB 241 LFWTYPYVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFR 300  
 QY 314 RYLSVFERKHITKRCCKQCFVRETVGVTSTNTPTSGQEVSAKL 360  
 DB 301 RYLSVFERKHITKRCCKQCFVRETVGVTSTNTPTSGQEVSAKL 347

## RESULT 12

AAR79165

ID AAR79165 standard; protein; 374 AA.

XX AC AAR79165;

XX DT 25-MAR-2003 (revised)

XX DT 29-DEC-1995 (first entry)

XX DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.

XX KW Monocyte chemoattractant protein-1 receptor; MCP-1R; chemokine.

XX OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Domain 1..48  
 FT /label= extracellular  
 FT Domain 49..70  
 FT /label= transmembrane  
 FT Domain 80..700  
 FT /label= transmembrane  
 FT Domain 115..136  
 FT /label= transmembrane  
 FT Domain 154..178  
 FT /label= transmembrane  
 FT Domain 204..231  
 FT /label= transmembrane  
 FT Domain 244..268  
 FT /label= transmembrane  
 FT Domain 295..313  
 FT /label= transmembrane  
 FT Region 314..375  
 FT /label= carboxyl tail

XX WO9519436-A1.

XX XX 20-JUL-1995.

XX XX 11-JAN-1995; 95WO-US000476.

XX XX 13-JAN-1994; 94US-00182962.

XX XX (REGC ) UNIV CALIFORNIA.

XX XX Charo I, Coughlin S;

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

DR WPI; 1995-263866/34.

XX N-PSDB; AAQ96297.

XX DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.

XX PT for identifying antagonists and for treating diseases characterised by

XX PS monocytic infiltrates.

XX XX Claim 2; Fig 1; 84pp; English.

XX CC To identify and clone new members of the chemokine receptor gene family,

XX CC degenerate oligo primers were designed corresp. to the conserved

XX CC sequences R79167 in the second and R79168 in the third transmembrane

XX CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the

XX CC HUMSTRS orphan receptor (GenBank Accession #M99293). The degenerate oligo

XX CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and

XX CC Q96300. Amplification of cDNA derived from MM6 cells with the primers

XX CC yielded a number of PCR products. One cDNA appeared to encode a novel

XX CC protein. To obtain a full-length version of this clone, a MM6 cDNA

XX CC library was constructed in pFROG and probed with the PCR product. A 2.1

XX CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA

XX CC library revealed a second sequence that was identical to the 2.1 kb cDNA

XX CC sequence first obtd. from the 5' UTR through the putative seventh

XX CC transmembrane domain but contained a different cytoplasmic tail. The

XX CC second sequence appears to represent alternative splicing of the carboxyl

XX CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-

XX CC 1RA and MCP-1RB (see Q96297/R79165 &amp; Q96298/R79166). Active mature MCP-

XX CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.

XX CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN

XX CC field.)

XX CC

XX SQ Sequence 374 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic.

OS Homo sapiens.

XX WO200172830-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IPFP-) IPF PHARM GMBH.

XX (FORS/) FORSSMANN U.

XX Forsemann W, Adermann K, Heitland A, Spodeberg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.

XX Disclosure; Page 9; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. CC Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, CC endocrine, motor or urogenital systems or skin are affected, and bone CC marrow diseases. The products of the invention are chemokine derivatives CC which have cytostatic, antiinflammatory, antirheumatic, antiarthritic. CC immunosuppressive, dermatological, antirheumatic, antiarthritic. CC Chemokines act on specific tumor and inflammatory cells through a CC constellation of chemokine receptors (CR), which control migration and CC proliferation of these cells. AAG8045-AAG8018 represent human chemokine CC fragments used to illustrate the method of the invention

XX SQ Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 4; Length 374;

Best Local Similarity 95.5%; Pred. No. 3.1e-178;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRFRFRNTNESGEVTFDDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60

Db 1 MLSTSRFRFRNTNESGEVTFDDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60

Qy 61 MLVVLILINCKKCLDIYLLNLAISDLLFLITPLWHAASANEWVFGNACKLFTGLY 120

Db 61 MLVVLILINCKKCLDIYLLNLAISDLLFLITPLWHAASANEWVFGNACKLFTGLY 120

Qy 121 HIGYFGGIFPILLITIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

Db 121 HIGYFGGIFPILLITIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

Qy 181 COKEDSVVCGPYPRGNFNFTIMRNILGLVPLLIWVICYSIGILTKLRCRNEKRRH 240

Db 181 COKEDSVVCGPYPRGNFNFTIMRNILGLVPLLIWVICYSIGILTKLRCRNEKRRH 240

Qy 241 AVRVIPTIMIVYFLWTPYNYVILLNTFQBFGLSNCESTSQLDOATQVTTGLMTHCCI 300

Db 241 AVRVIPTIMIVYFLWTPYNYVILLNTFQBFGLSNCESTSQLDOATQVTTGLMTHCCI 300

Qy 301 NPITIAVFGKFRYLSVFFRKHITKRCQCPV 334

Db 301 NPITIAVFGKFR---SLF---HIALG-CRIAPL 327

## RESULT 14

ABU09083

XX ABU09083 standard; protein; 374 AA.

XX AC ABU09083;

XX 23-JUL-2003 (first entry)

XX Human chemokine receptor-2 (CKR-2) polypeptide.

XX Human; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor; MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma; monocyte/dendritic cell receptor for chemokine; inflammatory condition; abnormal physiology; abnormal proliferation; degeneration; atrophy; antiinflammatory; antiasthmatic; cytostatic; chemokine receptor-2; CKR-2.

XX OS Homo sapiens.

XX US2003018167-A1.

XX 23-JAN-2003.

XX 03-JAN-2002; 2002US-00039659.

XX 05-JUL-1996; 96US-0021664P.

XX 11-OCT-1996; 96US-0028329P.

XX 04-JUN-1997; 97US-0048593P.

XX 03-JUL-1997; 97US-00887977.

XX (SCHE) SCHERING CORP.

XX Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;

XX WPI; 2003-416900/39.

XX New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions (e.g. asthma), and abnormal proliferation.

XX Disclosure; Page 9-10; 54pp; English.

XX The invention relates to nucleic acids encoding the chemokines TECK, MIP-3 alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are useful in isolating DNA clones encoding the chemokines, for generating antibodies, and for predicting oligonucleotides for screening a library to isolate species variants. A nucleic acid encoding a chemokine polypeptide can be used to identify genes, mRNA and cDNA species which encode related or homologous ligands, as well as DNA encoding homologous proteins from different species. The chemokines and antibodies which bind to the polypeptides are useful in the treatment of conditions associated with abnormal physiology or development, including inflammatory conditions such as asthma, abnormal proliferation, regeneration, degeneration and atrophy. This sequence represents the human chemokine receptor-2 (CKR-2) polypeptide, used in the scope of the invention

XX SQ Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 6; Length 374;

Best Local Similarity 95.5%; Pred. No. 3.1e-178;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRFRFRNTNESGEVTFDDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60

Db 1 MLSTSRFRFRNTNESGEVTFDDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60

Qy 61 MLVVLILINCKKCLDIYLLNLAISDLLFLITPLWHAASANEWVFGNACKLFTGLY 120

Db 61 MLVVLILINCKKCLDIYLLNLAISDLLFLITPLWHAASANEWVFGNACKLFTGLY 120

Qy 121 HIGYFGGIFPILLITIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

Db 121 HIGYFGGIFPIILLTIDRYLAIVHAFVPAKARTVTFGWTSVITLWVAFASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYPPRGWNNFHTMRNIGLVLPPLIMVICYSGILKTLRCNEKKRHR 240  
Db 181 CQKEDSVYVCGPYPPRGWNNFHTMRNIGLVLPPLIMVICYSGILKTLRCNEKKRHR 240  
QY 241 AVRVIETIMIVYFLWTPYNIIVLLNTFQFFGLSNCESTSOLDQATQVETLGMTHCCI 300  
Db 241 AVRVIETIMIVYFLWTPYNIIVLLNTFQFFGLSNCESTSOLDQATQVETLGMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPV 334  
Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 15  
ADD44861  
ID ADD44861 standard; protein; 374 AA.  
XX AC ADD44861;  
XX DT 29-JAN-2004 (first entry)  
XX DE Human Protein P41597, SEQ ID NO 10292.  
XX KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX OS Homo sapiens.  
XX WQ2003016475-A2.  
XX PN 27-FEB-2003.  
XX PF 14-AUG-2002; 2002WO-US025765.  
XX PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
XX 26-NOV-2001; 2001US-0333347P.  
XX (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX Woolf C, D'urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
DR GENBANK; P41597.  
XX PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 7; Length 374;  
Best Local Similarity 95.5%; Pred. No. 3.1e-178;  
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;  
QY 1 MLSTSRSRFIRNTNESGEEVTPFDYDGAPCHKFDVKQIGAQLLPPLSLVIFGFGVN 60  
Db 1 MLSTSRSRFIRNTNESGEEVTPFDYDGAPCHKFDVKQIGAQLLPPLSLVIFGFGVN 60  
QY 61 MLVVLILINCKKLCUTDIYLLNLAIISDLLFLITLPLMAHSAANWVFGNAMCKLFTGLY 120  
Db 61 MLVVLILINCKKLCUTDIYLLNLAIISDLLFLITLPLMAHSAANWVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAFVPAKARTVTFGWTSVITLWVAFASVPGIIFTK 180  
Db 121 HIGYFGGIFPIILLTIDRYLAIVHAFVPAKARTVTFGWTSVITLWVAFASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYPPRGWNNFHTMRNIGLVLPPLIMVICYSGILKTLRCNEKKRHR 240  
Db 181 CQKEDSVYVCGPYPPRGWNNFHTMRNIGLVLPPLIMVICYSGILKTLRCNEKKRHR 240  
QY 241 AVRVIETIMIVYFLWTPYNIIVLLNTFQFFGLSNCESTSOLDQATQVETLGMTHCCI 300  
Db 241 AVRVIETIMIVYFLWTPYNIIVLLNTFQFFGLSNCESTSOLDQATQVETLGMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPV 334  
Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

Search completed: June 9, 2005, 16:44:16  
Job time : 112.826 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:29:43 ; Search time 25.0136 Seconds  
(without alignments)  
1384.767 Million cell updates/sec

Title: US-10-791-166-4

Perfect score: 1900

Sequence: 1 MLSTSRGRPRINTNESGEV.....DGVTSNTPTSGGEVSAGL 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1900	100.0	360	2 JC2443	chemokine (C-C) re
2	1651.5	86.9	374	2 I38450	chemokine (C-C) re
3	1364	71.8	352	2 A43113	chemokine (C-C) re
4	1036	54.5	355	2 A45177	chemokine (C-C) re
5	1010.5	53.2	359	2 I49341	Mip-1 alpha recept
6	963.5	50.7	355	2 I49339	macrophage inflamm
7	951	50.1	355	2 G02436	chemokine (C-C) re
8	871	45.8	360	2 JC4587	chemokine (C-C) re
9	862.5	45.4	360	2 A57160	chemokine (C-C) re
10	822.5	43.3	383	2 S55594	G protein-coupled
11	778.5	41.0	356	2 I49340	Mip-1 alpha recept
12	751	39.5	355	2 JC5067	G protein-coupled
13	722.5	38.0	354	2 I58186	chemokine (C-C) re
14	708	37.3	355	2 JC4304	orphan G protein-c
15	649.5	34.2	344	2 JC5942	chemokine receptor
16	581.5	30.6	378	2 B55735	lymphocyte-specifi
17	569	29.9	378	2 A55735	G protein-coupled
18	567.5	29.9	378	2 A55680	G protein-coupled
19	563	29.6	369	2 JC5068	G protein-coupled
20	547	28.8	360	2 A53611	interleukin-8 rece
21	540.5	28.4	355	2 J01231	interleukin-8 rece
22	540.5	28.4	359	2 A48921	interleukin-8 rece
23	536.5	28.0	358	2 A53752	interleukin-8 rece
24	532.5	28.0	356	2 S42096	interleukin-8 rece
25	532	28.0	367	2 J80349	interferon-inducib
26	528.5	27.8	333	2 I65989	G protein-coupled
27	528.5	27.8	350	2 A39445	interleukin-8 rece
28	515.5	27.1	352	2 G00048	fusin (LSTRA) - c
29	515	27.1	353	2 S28787	neuropeptide Y/pep

ALIGNMENTS

RESULT 1

JC2443

chemokine (C-C) receptor 2, splice form B - human

N/Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem

C/Species: Homo sapiens (man)

C/Date: 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004

C/Accession: JC2443; I38463

R/Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.

Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994

A/Title: cDNA cloning and functional expression of a human monocyte chemoattractant prote

A/Reference number: JC2443; MUID:94324942; PMID:8048929

A/Accession: JC2443

A/Molecule type: mRNA

A/Residues: 1-360 <YAM>

A/Cross-references: UNIPROT:P41597; DBJ:D29984; NID:G531246; PIDN:BAA06253.1; PID:G53124

R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A/Title: Molecular cloning and functional expression of two monocyte chemoattractant prot

A/Reference number: A53477; MUID:94195821; PMID:8146186

A/Accession: I38463

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-360 <RES>

A/Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558

C/Genetics:

A/Gene: GDB:CMKBR2

A/Cross-references: GDB:337364; OMIM:601267

A/Map position: 3p21-3p21

C/Superfamily: vertebrate rhodopsin

C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane

F:43-70/Domain: transmembrane #status predicted <TM1>

F:81-100/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:154-178/Domain: transmembrane #status predicted <TM4>

F:207-226/Domain: transmembrane #status predicted <TM5>

F:244-268/Domain: transmembrane #status predicted <TM6>

F:287-309/Domain: transmembrane #status predicted <TM7>

F:14/Binding site: carbohydrate (Aen) (covalent) #status predicted

F:113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1900; DB 2; Length 360;

Best Local Similarity 100.0%; Pred. No. 1.6e-156;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRGRPRINTNESGEVTFPDYDYGAPCHFDVKQIGAQQLLPPLYSLVFIFFGVGN 60

Db 1 MLSTSRGRPRINTNESGEVTFPDYDYGAPCHFDVKQIGAQQLLPPLYSLVFIFFGVGN 60

Qy 61 MLVVLILNCKKLCITDIYLLNLAISDLLPLITLPLWAHSAANWVFGNWKLTGLY 120

Db 61 MLVVLILNCKKLCITDIYLLNLAISDLLPLITLPLWAHSAANWVFGNWKLTGLY 120

neuropeptide Y/pep  
G protein-coupled  
angiotensin II rec  
angiotensin II rec  
angiotensin II rec  
G protein-coupled  
angiotensin II rec  
angiotensin II rec  
angiotensin II rec  
angiotensin II rec  
angiotensin II rec  
angiotensin II rec  
angiotensin II rec  
angiotensin II rec  
G protein-coupled  
MDCR15 protein - h  
G protein-coupled

30 512.5 27.0 352 2 A45747  
31 495.5 26.1 350 2 JN0621  
32 486.5 25.6 359 2 S15403  
33 480.5 25.3 359 2 A42656  
34 480 25.3 374 2 S42628  
35 475.5 25.0 359 2 JC2134  
36 474.5 25.0 359 2 JC1104  
37 474.5 25.0 359 2 S44425  
38 472.5 24.9 359 2 JH0621  
39 471.5 24.8 359 2 JQ1516  
40 469.5 24.7 359 2 JC1194  
41 468.5 24.7 359 2 I51372  
42 466 24.5 359 2 A48857  
43 465.5 24.5 374 2 S32785  
44 465 24.5 327 2 S56162  
45 465 24.5 372 2 S26667

121 HIGVFGGIFPIILLTIDRYLAIVHVPALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 121 HIGVFGGIFPIILLTIDRYLAIVHVPALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 181 COKEDSVVCGPVFPRGNNPHITMRNLGLVPLLMVICYSGILKTLRCRNEKKRHR 240  
 181 COKEDSVVCGPVFPRGNNPHITMRNLGLVPLLMVICYSGILKTLRCRNEKKRHR 240  
 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 301 NPIIYAVGKFRYLSVFFRKHTKFCQCPVYFRETVDGVTSTWTPSTGEOVSAGL 360  
 301 NPIIYAVGKFRYLSVFFRKHTKFCQCPVYFRETVDGVTSTWTPSTGEOVSAGL 360

RESULT 2  
 I38450  
 chemokine (C-C) receptor 2, splice form A - human  
 N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004  
 C;Accession: I38450  
 R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
 A;Title: Molecular cloning and functional expression of two monocyte chemoattractant pro  
 A;Reference number: A53477; MUID:94195821; PMID:8146186  
 A;Accession: I38450  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-374 <RES>  
 A;Cross-references: UNIPROT:P41597; EMBL:U03882; NID:G472555; PIDN:AAA19119.1; PID:G4725  
 C;Genetics:  
 A;Gene: GDB:CMKBR2  
 A;Cross-references: GDB:337364; OMIM:601267  
 A;Map position: 3p21-3p21  
 C;Superfamily: vertebrate rhodopsin  
 F;44-68/Domain: transmembrane #status predicted <TM1>  
 F;79-99/Domain: transmembrane #status predicted <TM2>  
 F;115-136/Domain: transmembrane #status predicted <TM3>  
 F;154-178/Domain: transmembrane #status predicted <TM4>  
 F;208-226/Domain: transmembrane #status predicted <TM5>  
 F;244-265/Domain: transmembrane #status predicted <TM6>  
 F;292-309/Domain: transmembrane #status predicted <TM7>  
 F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;32-277,113-190/bisulfide bonds: #status predicted

Query Match 86.9%; Score 1651.5; DB 2; Length 374;  
 Best Local Similarity 95.5%; Pred. No. 4.8e-135;  
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSFIRNTNSESBEVTFPDYDYGAPCHKFDVKQIGCAQLLPPLYSLVFIPIFGVGN 60  
 Db 1 MLSTSRSFIRNTNSESBEVTFPDYDYGAPCHKFDVKQIGCAQLLPPLYSLVFIPIFGVGN 60  
 61 MLVLLINCKKLKCLTDIYLLNLAISSDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120  
 61 MLVLLINCKKLKCLTDIYLLNLAISSDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120  
 121 HIGVFGGIFPIILLTIDRYLAIVHVPALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 121 HIGVFGGIFPIILLTIDRYLAIVHVPALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 181 COKEDSVVCGPVFPRGNNPHITMRNLGLVPLLMVICYSGILKTLRCRNEKKRHR 240  
 181 COKEDSVVCGPVFPRGNNPHITMRNLGLVPLLMVICYSGILKTLRCRNEKKRHR 240  
 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300

Qy 301 NPIIYAVGKFRYLSVFFRKHTKFCQCPV 334  
 Db 301 NPIIYAVGKFR---SLF---HIALG-CRIAPL 327

RESULT 3  
 A43113  
 chemokine (C-C) receptor 5 - human  
 N;Alternate names: C-C CKR-5; CCR5  
 C;Species: Homo sapiens (man)  
 C;Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 20-Jun-2000  
 C;Accession: A43113; S71808; A58834; A58832; G02653; A58833  
 R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.  
 Biochemistry 35, 3362-3367, 1996  
 A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor  
 A;Reference number: A43113; MUID:96241590; PMID:8639485  
 A;Accession: A43113  
 A;Molecule type: mRNA  
 A;Residues: 1-352 <SAM1>  
 A;Cross-references: GB:X91492; NID:G1262810; PIDN:CAA62796.1; PID:G1262811  
 R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti  
 M.; Inai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Par  
 Nature 382, 722-725, 1996  
 A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of  
 A;Reference number: S71808; MUID:96345670; PMID:8751444  
 A;Accession: S71808  
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 182-206;207-230 <SAM2>  
 A;Accession: A58834  
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-184,'IKDSHLGAGPAAAGHLLGNPKNSASVSK' <SAM3>  
 A;Cross-references: GB:X99393; NID:G1524062; PIDN:CAA67767.1; PID:G1524063  
 A;Note: This frameshift mutation results in a non-functional receptor but confers a degree  
 nd may have had a selective advantage by conferring resistance to Yersinia plague infecti  
 R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.  
 J. Leukoc. Biol. 60, 147-152, 1996  
 A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rece  
 A;Reference number: A58832; MUID:96295970; PMID:8699119  
 A;Accession: A58832  
 A;Molecule type: mRNA  
 A;Residues: 1-352 <COM1>  
 A;Cross-references: GB:U57840; NID:G1502408; PIDN:AAB17071.1; PID:G1502409  
 A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
 R;Combadiere, C.  
 submitted to the EMBL Data Library, May 1996  
 A;Reference number: H01541  
 A;Accession: G02653  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-89,'L',91-352 <COM2>  
 A;Cross-references: EMBL:U57840  
 R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.  
 J. Biol. Chem. 271, 17161-17166, 1996  
 A;Title: Molecular cloning and functional characterization of a novel human CC chemokine  
 A;Reference number: A58833; MUID:96291862; PMID:8663314  
 A;Accession: A58833  
 A;Molecule type: mRNA  
 A;Residues: 1-352 <RAP>  
 A;Cross-references: GB:U54994; NID:G1457945; PIDN:AAC50598.1; PID:G1457946  
 C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see  
 C;Keywords: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C  
 C;Genetics:  
 A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13  
 A;Cross-references: GDB:1230510; OMIM:601373  
 A;Map position: 3p21-3p21  
 C;Function:  
 A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES  
 A;Note: probably acts to control granulocyte proliferation and differentiation  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane  
 F;32-56/Domain: transmembrane #status predicted <TM1>

```

F:67-87/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>
F:142-166/Domain: transmembrane #status predicted <TM4>
F:193-218/Domain: transmembrane #status predicted <TM5>
F:236-257/Domain: transmembrane #status predicted <TM6>
F:285-300/Domain: transmembrane #status predicted <TM7>
F:20-269,101-178/disulfide bonds: #status predicted
F:268/Binding site: carboxylate (Asn) (covalent) #status predicted
F:336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F:340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match          71.8%; Score 1364; DB 2; Length 352;
Best Local Similarity 75.5%; Pred. No. 3e-110;
Matches 259; Conservative 32; Mismatches 46; Indels 6; Gaps 2;

Qy      24  FDYDY--GAPCHKFDVQIGQALLPPYLSLVIFGFVGNMLVLILINCKLKCLTDIYL 81
Db      10  YDINYYTSEPCKINVKQAARLLPPYLSLVIFGFVGNMLVLILINCKLKLSMTDIYL 69

Qy      82  LNTAISDLPLILTLPLWAHSAANEWFEGNAMCKLFTGLYHIGYEGGIFFIILLTIDRYLA 141
Db      70  LNTAISDLFFLLTVPFWAHYAAAQWDFGNTWCQLTGLTYFIGFSGIFFIILLTIDRYLA 129

Qy      142  IVHAVFALKARTVTFGVVTSVITLWVAEASVPGIIFTKCKEDSVVVCGPYP-----RG 197
Db      130  VHAVFALKARTVTFGVVTSVITWVAVASLPGIILFRSQEGLHLYTCSHSPYSQYQF 189

Qy      198  WNNPHTIMRNILGLVLPALLINVICYSGILKATLLRCNEKKRHRVAVIFIMTVYFLFWT 257
Db      190  WKNPQTLKIVLGLVLPVWVICYSGILKATLLRCNEKKRHRVAVLIFIMIVYFLFWA 249

Qy      258  PYNIVILLNTFOEPFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRYLS 317
Db      250  PYNIVILLNTFOEPFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFVGEKFRNYLL 309

Qy      318  VFRKHHITKPCCKCPYFARTVDGVTSTWTPSTGEOEVSAGL 360
Db      310  VFFOKHIAKFCCKCSITFOEAPERASSVYTRSTGEOEISVGL 352

```

RESULT 4

A45177  
chemokine (C-C) receptor 1 - human  
N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: A45177; I55671  
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.  
Cell 72, 415-425, 1993  
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor  
A;Reference number: A45177; MUID:93161416; PMID:7679328  
A;Accession: A45177  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-355 <NRO>  
A;Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417  
A;Experimental source: HL60 cells  
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)  
R;Gao, J.  
J. Exp. Med. 177, 1421-1427, 1993  
A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha chemokine receptor  
A;Reference number: I55671; MUID:93240122; PMID:7683036  
A;Accession: I55671  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-355 <RES>  
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417  
C;Genetics:  
A;Gene: GDB:CMKBR1; CMKR-1  
A;Cross-references: GDB:i38446; OMIM:601159  
A;Map position: 3p21-3p21  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; trypsin

```

F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-264/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:5/Binding site: carbohydurate (Aan) (covalent) #status predicted
F:24-273,106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match          54.5%; Score 1036; DB 2; Length 355;
Best Local Similarity 56.4%; Pred. No. 6.4e-82;
Matches 199; Conservative 56; Mismatches 90; Indels 8; Gaps 5;

Qy 12 NTNESGEVTTFFDYDGAPCHFDVKQIGAOQLLPPLYSLVFIQFVGNMLVLINCK 71
Db 5 NTTED-VDTTTFDYGDATPCQKNERAFQALLPPLYSLVFIQFVGNMLVLINCK 63

Qy 72 KLKCLTDIYLINLAISDLLFLITPLWA-HSANEWFGNAMCKLFLGLVHIGFGGIFP 130
Db 64 RLKNMITSYLLNLAISDLLFLTPWFIDYKLKDDWFGDMCKILSGFYTGLYSIFF 123

Qy 131 ILLLTIDRYLAIHVAVFALKARTVTCGVTSVITLWAVFASVPGIIFTCKEDSVYVC 190
Db 124 ILLLTIDRYLAIHVAVFALKARTVTCGVTSVITLWAVFASVPGIIFTCKEDSVYVC 183

Qy 191 GPVFP-----RGWNFFHTIMENILGLVPLLIWICYSGILKTLRLCRNEKKRHRAVRVF 246
Db 184 SLHPFHESLEWKLFOALKLNLGLVLPLVMIICYTGIIKILLRRNEKK-SKAVRLIF 242

Qy 247 TIMIVFLFTPNYVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCINPIYA 306
Db 243 VIMIIFLFTPNYVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCINPIYA 302

Qy 307 FVGEKFRRLYSVFRKHTIKRQCKQPVFRETVDGVTSTNTPTSGEQEVSAG 359
Db 303 FVGEKFRKRLQLFHRRVAVHLVKMLPFLSVDRLEVRVST-SPSTGEHLSAG 355

```

```

RESULT 5
I49341
MIP-1 alpha receptor like-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49341
E:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemok
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49341
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A:Cross-references: UNIPROT:Q9K3M7; EMBL:U28406; NID:g881551; PID:g881552
C:Superfamily: vertebrate rhodopsin

Query Match      Score 1010.5; DB 2; Length 359;
Best Local Similarity 53.2%; Pred. No. 1e-79;
Matches 193; Conservative 62; Mismatches 81; Indels 25; Gaps 6;

Qy      10  IRNTNSESGETVTFDDYDYGACPKEDVKQIGAQQLLPPLYSLSVPIFGVGNMLVVLIN 69
Db      8  IKTWVESFE--FTPYEYEWAPCCPKRYKESGLWLLPPLYSLSVPIIIGLGNMVMVILIK 65

Qy      70  CKKLKCLITDYLNLALISDLLFLITPLWAHSAA-NEWVFGNAMCKLFTGLYHIGYFGGI 128
Db      66  YRKLQIMTNIYLFNLALISDLLFLFTVPFPIHYVLWNWEGFGHYMCKMLSGFYLYALYSEI 125

Qy      129  FFIILLTIDRYLAIVHAVPALKARTTTFGVVTSVITWLVAVPASVPGIIFTKCKEDSVY 188
Db      126  FFIILLTIDRYLAIVHAVPALRARTVTFATITSITWGLAGLAALPEFIFHESQDSFGEF 185

```

Qy 189 VCGPYFRG-----WNNFHTIMRNILGLVPLLLIMVICYSGILKTLRLCRNEKKHRAVRV 244  
 Db 186 SCSRYPEGEEDSKWRFAHARNVIFGLALPLLVVICYSGIITKLLRCNP-KKKHKAIRL 244  
 Qy 245 IFTIMVFLFWTPYNIIVILLNTFOEPFGLSNCESTSDQATQVTLGTHCCINPII 304  
 Db 245 IFVMIVFETWTPYNLVLLSFAHSITFLESQSKHLDLMAQVTEVIATHCVCNPEVI 304  
 Qy 305 YAFVGEKPRRYLSVFFRKHTKTRFCQCPVYRETV-----DGVSTWTPSTGBOEV 356  
 Db 305 YAFVGERPRKHLRLFHRNVQ-----FTWENIFQFLPGEENGRTSSVSPSTGBOEI 355  
 Qy 357 S 357  
 Db 356 S 356

RESULT 6  
 149339  
 macrophage inflammatory protein-1 alpha receptor - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I49339  
 R:Gao, J.L.; Murphy, P.M.  
 J. Biol. Chem. 270, 17494-17501, 1995  
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine  
 A:Reference number: I49339; MUID:953440546; PMID:7542241  
 A:Accession: I49339  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-355 <RES>  
 A:Cross-references: UNIPROT:P51675; EMBL:U28404; NID:9881547; PIDN:AAA89153.1; PID:98815  
 C:Superfamily: vertebrate rhodopsin

Query Match 50.7%; Score 963.5; DB 2; Length 355;  
 Best Local Similarity 52.3%; Pred. No. 1.2e-75;  
 Matches 181; Conservative 65; Mismatches 89; Indels 11; Gaps 5;  
 Qy 21 TTFDFDYDYGAPCHKFDVKQIGQALLPPLYSLVIFGFGVGNMVLVLLINCKKJLCITDIY 80  
 Db 13 TTFDFDYGSTPCKTAVRAFGAGLLPPLYSLVIFGFGVGNMVLVLLINCKKJLCITDIY 72  
 Qy 81 LNLAIISDLLPLITPLWAHSA-ANEWVFGNMAKCLFGLVHIGYFGGIFFIILLTDIY 139  
 Db 73 LNLAVSGLVFLTLFPFIDYKLDKDDWIFGDAMCKLLSGFYLLGYSEIFFIILLTDIY 132  
 Qy 140 LAIVHAVFALKARTVTGCVTSVITLWVAVFASVPGIIFTCKQKEDSVVVCVPYPP---- 195  
 Db 133 LAIVHAVFALKARTVTGLIISITWAILASMPALYFFKAQWFTHTCSPHPYKSL 192  
 Qy 196 RGNWFHTIMRNILGLVPLLLIMVICYSGILKTLRLCRNEKKHRAVRVIFTIMIVYFLF 255  
 Db 193 KQWRFQALKNLLGLILPLLWMIICYAGIIRLLR-RPSEKKVAVRLIFAITLLFLL 251  
 Qy 256 WTPYNIIVILLNTPQFFGLSNCESTSDQATQVTLGTHCCINPIIYAFVGEKPRRY 315  
 Db 252 WTPYNLVSVFAFDVLFNQCEQSKHLDLMAQVTEVIATHCVCNPIIYFVGERFWKY 311  
 Qy 316 LSVFRKHITKRFCKQCPVYRETVDGV--TSNTPTSTGBOEVASG 359  
 Db 312 LRQLFQRHVAIPLAKWLPLF---SVDQLERTSSISPSGHEHLSAG 354

RESULT 7  
 G02436  
 chemokine (C-C) receptor 3 - human  
 N:Alternate names: C-C CKR-3  
 C:Species: Homo sapiens (man)  
 C>Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
 A:Reference number: G02436; A57237  
 R:Ponath, P.D.  
 submitted to the EMBL Data Library, February 1996  
 A:Reference number: H01272

A:Accession: G02436  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-355 <PON>  
 A:Cross-references: UNIPROT:P51677; EMBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477  
 R:Combadieze, C.; Ahuja, S.K.; Murphy, P.M.  
 J. Biol. Chem. 270, 16491-16494, 1995  
 A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.  
 A:Reference number: A57237; MUID:95348056; PMID:7622448  
 A:Accession: A57237  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-106 'N', 108-275 'S', 277-280 'R', 282-355 <COM>  
 A:Cross-references: GB:U28694; NID:gl1199579; PIDN:AAC50469.1; PID:gl1199580  
 A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1  
 C:Genetics:

A:Gene: GDB:CMKBR3  
 A:Cross-references: GDB:579624; OMIM:601268  
 A:Map position: 3p21-3p21  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote  
 F:36-60/Domain: transmembrane #status predicted <TM1>  
 F:71-91/Domain: transmembrane #status predicted <TM2>  
 F:108-129/Domain: transmembrane #status predicted <TM3>  
 F:147-171/Domain: transmembrane #status predicted <TM4>  
 F:205-223/Domain: transmembrane #status predicted <TM5>  
 F:240-261/Domain: transmembrane #status predicted <TM6>  
 F:288-305/Domain: transmembrane #status predicted <TM7>  
 F:24-273,106-183/Disulfide bonds: #status predicted  
 F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 50.1%; Score 951; DB 2; Length 355;  
 Best Local Similarity 52.6%; Pred. No. 1.4e-74;  
 Matches 180; Conservative 65; Mismatches 89; Indels 8; Gaps 5;  
 Qy 21 TTFDFDYDYGAPCHKFDVKQIGQALLPPLYSLVIFGFGVGNMVLVLLINCKKJLCITDIY 80  
 Db 14 TSYDYD-DVGLLCEKADTRALMAQFVPLYSVFTVGLLGNVVMILIKYRLRIMTNY 72  
 Qy 81 LNLAIISDLLPLITPLWAHSA-ANEWVFGNMAKCLFGLVHIGYFGGIFFIILLTDIY 139  
 Db 73 LNLAIISDLLPLITPLFPMIHYVRGNWVFGMKLLSGFYHTGLYSIFFIILLTDIY 132  
 Qy 140 LAIVHAVFALKARTVTGCVTSVITLWVAVFASVPGIIFTCKQKEDSVVVCVPYPPR--- 196  
 Db 133 LAIVHAVFALKARTVTGCVTSVITLWVAVFASVPGIIFTCKQKEDSVVVCVPYPPR 192  
 Qy 197 -GWNFHTIMRNILGLVPLLLIMVICYSGILKTLRLCRNEKKHRAVRVIFTIMIVYFLF 255  
 Db 193 YSRHFHTLRMTIFCLVPLLVMAICYGTGIITLLRCPS-KKKYKAIRLIIFVIMAVFFIF 251  
 Qy 256 WTPYNIIVILLNTPQFFGLSNCESTSDQATQVTLGTHCCINPIIYAFVGEKPRRY 315  
 Db 252 WTPYNAVILLSYQISILFGNDCERTKHLDLVMLVTEVIATHCVCNPIIYAFVGERFRKY 311  
 Qy 316 LSVFRKHITKRFCKQCPVYRETVDGVTSNTPTSTGBOEVS 357  
 Db 312 LRHFFRHLMLHGLGRYIPFLPSEKLER-TSSVSFSTAPPELS 352

RESULT 8  
 JC4587  
 chemokine (C-C) receptor 4 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
 C:Accession: JC4587  
 R:Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.  
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996  
 A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to  
 A:Reference number: JC4587; MUID:96136324; PMID:8573157  
 A:Accession: JC4587  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <HOO>



A:Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167851  
A:Experimental source: thymus  
C:Genetics:  
A:Gene: cc ckr-4  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus  
F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted  
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.8%; Score 871; DB 2; Length 360;  
Best Local Similarity 47.5%; Pred. No. 1.1e-67;  
Matches 168; Conservative 71; Mismatches 103; Indels 12; Gaps 5;  
QY 10 INTNESGEVTTFFDYD-YGAPCHKFDVKQIGCAQLLPPLYSLVIFGFGVGNMVLVLI 68  
DB 6 VTDITQDETIVNSYVYFESMPKPCFKGKAFGEVFLPPLYSLVIFGFGVGNMVLVLF 65  
QY 69 NCKLKLCLTDIYLNLAISDLFLTLPLWAHSAANWFGNAMCKLFTGLYHIGYFGGI 128  
DB 66 KYRLKLSMTDVLNLAISDLFLVLSLPFGWGYAADQWVFGGLCKIVSNWVYLVGYSGI 125  
QY 129 PFILITLDYLAIVHAFKARTVFGVTSVITLWVAFASVPGIIFTKCKEDSVY 188  
DB 126 PFILMSIDRYLAIVHAFSLKARTLVITSLITWVAFASVPGIIFTKCKEDSVY 185  
QY 189 VCGPYF---PGWNNFHTIMRNILGLVPLLMVICYSGLKTLRCNEKRRHRAVRVI 245  
DB 186 YCKTQYSVNSTTKVLSLEINVLGLLPLGIMLFWYSMIITLQCKNEKK-NRAVRMI 244  
QY 246 FTIMIVFLFTPPYNNVILLNTQBFGLSNCESTSOLDQATQVTTGLMTHCCINPIIY 305  
DB 245 FGWVFLGFWTPYNNVLFLETLVEVLQDCTERYLDYAIQATETLGFHCCINPVII 304  
QY 306 APVGEKFRYLSVFRKHITKR----FCKQCPVFRVETDGVTSNTFTSTGEOE 355  
DB 305 PFLGEBKFRYITQLFR---TCRGLVLCKHDFLQVYADSMSSSYTOSTVDHD 355

RESULT 9  
A57160  
Chemokine (C-C) receptor 4 - human  
N:Alternate names: C-C CKR-4  
C:Species: Homo sapiens (man)  
C:Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: A57160  
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W  
J. Biol. Chem. 270, 19495-19500, 1995  
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor c  
A:Reference number: A57160; MUID:95370289; PMID:7642634  
A:Accession: A57160  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-360 <POM>  
A:Cross-references: UNIPROT:P51679; GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g97145  
A:Note: source clone K5-5  
C:Genetics:  
A:Gene: GDB:CMKBR4  
A:Cross-references: GDB:677463  
A:Map position: 3p21-3p21  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot  
F:40-65/Domain: transmembrane #status predicted <TM1>  
F:76-97/Domain: transmembrane #status predicted <TM2>  
F:112-133/Domain: transmembrane #status predicted <TM3>  
F:151-175/Domain: transmembrane #status predicted <TM4>  
F:208-226/Domain: transmembrane #status predicted <TM5>  
F:243-264/Domain: transmembrane #status predicted <TM6>  
F:291-308/Domain: transmembrane #status predicted <TM7>  
F:29-276,110-187/disulfide bonds: #status predicted  
F:72,350/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted  
F:145/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.4%; Score 862.5; DB 2; Length 360;  
Best Local Similarity 48.7%; Pred. No. 6.1e-67;  
Matches 164; Conservative 67; Mismatches 95; Indels 11; Gaps 4;  
QY 31 PCKHFDVKQIGCAQLLPPLYSLVIFGFGVGNMVLVILINCKLCLTDIYLNLAISDLL 90  
DB 28 PCKEGIKAFGBLFLPPLYSLVIFGFGVGNMVLVILVLFKYKELRSMTDVLNLAISDLL 87  
QY 91 FLITLPLWAHSAANWFGNAMCKLFTGLYHIGYFGGIPIILLITLDYLAIVHAFK 150  
DB 88 FVPSLFPFGGYAADQWVFGGLCKMISWVYLVFGYSGIIFVNMISIDRYLAIVHAFS 147  
QY 151 ARTVTFGVVTSVITLWVAFASVPGIIFTKCKEDSVYVCGPYFPRG---WNNFHTIMRN 207  
DB 148 ARTLVGYVITSLATWSVAFASVPGIIFTKCKEDSVYVCGPYFPRG---WNNFHTIMRN 207  
QY 208 ILGLVPLLMVICYSGLKTLRCNEKRRHRAVRVITIMIVFLFTPPYNNVILLNT 267  
DB 208 ILGLVPLGIMLFCYSMIITLQCKNEKK-NKAVKMFVAVVFLGFWTPYNNVILFET 266  
QY 268 PQEPFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVCEKERRYSVFRKHITKR 327  
DB 267 LVELEVLQDCTERYLDYAIQATETLAFVHCCINPIIYFGLGERPKRYLQFK---TCR 323  
QY 328 ---FCKQCPVFRVETDGVTSNTFTSTGEOEVSAGL 360  
DB 324 GLFVLCCVCGLLQIYSADTPSSSYTOSTVDHDLHAL 360

RESULT 10  
S55594  
G protein-coupled receptor E1 - equine herpesvirus 2  
C:Species: equine herpesvirus 2  
C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: S55594  
R:Teiford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
J. Mol. Biol. 249, 520-528, 1995  
A:Title: The DNA sequence of equine herpesvirus 2.  
A:Reference number: S55594; MUID:95302501; PMID:7783207  
A:Accession: S55594  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-383 <TEL>  
A:Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor

Query Match 43.3%; Score 822.5; DB 2; Length 383;  
Best Local Similarity 47.9%; Pred. No. 1.9e-63;  
Matches 162; Conservative 60; Mismatches 107; Indels 9; Gaps 4;  
QY 4 TSSRFIRNTNESGEVTTFFDYD--GAPCHKFDVKQIGCAQLLPPLYSLVIFGFGVNM 61  
DB 32 TTIASLVPSSTSSDYDDLDVDYVESAPCVKSDTTLAAQWVPALYLLVFLGLGNI 91  
QY 62 LVVLLINCKLCLTDIYLNLAISDLFLTLPLWAH---SAANWFGNAMCKLFTGL 119  
DB 92 LVWIVIRYMKIKNLTNMLNLAISDLFLTLPLWAH---SAANWFGNAMCKLFTGL 151  
QY 120 YHIGVGGIPIILLITLDYLAIVHAFKARTVFGVTSVITLWVAFASVPGIIFT 179  
DB 152 CYMSLYSQVFCILLTVDRYLAIVHAFKARTVFGVTSVITLWVAFASVPGIIFT 211  
QY 180 KCQKEDSVYVCGPYF---RGWNNFHTIMRNILGLVPLLMVICYSGLKTLRCNE 235  
DB 212 GHODNGRVQCDPVYPEMSTNVWRAHVAKVIIMLSLILPLLIMAVCYVYVIRRLLR-RPS 270  
QY 236 KRRHRAVRVITIMIVFLFTPPYNNVILLNTQBFGLSNCESTSOLDQATQVTTGLM 295  
DB 271 KKKYKAIKRLIEIVWVAFVFWTPYNNVILLNTQBFGLSNCESTSOLDQATQVTTGLM 330

```

Qy      296  THCCINPIIYAFVGEKFRRLYSVEFRKHITKRECKQCP 333
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      331  THCCINPVIYAFVGEKFRRLHYHFFHTYVAIYLCKYIP 368

RESULT 11
I49340
MIP-1 alpha receptor like-1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49340
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokini
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49340
A>Status: preliminary; translated from GB/EMBL/DBDB
A:Molecule type: DNA
A:Residues: 1-356 <RES>
A:Cross-references: UNIPROT:P51676; EMBL:U28405; NID:g881549; PIDN:AA89154.1; PID:g8815
C:Superfamily: vertebrate rhodopsin

```

	Query Match	41.0%;	Score	778.5;	DB 2;	Length	356;			
	Best Local Similarity	45.2%;	Pred. No.	1.1e-59;						
	Matches	154;	Conservative	62;	Mismatches	118;	Indels	7;	Gaps	4
Qy	25	DYDYGAPCHKFDVQIGAGQAQLPPLYSLSLVIFGFGVGNMLVLILINCKKLCLTIDYLNL	84	:	:	:	:	:	:	:
Db	18	DFMSGFLCFSINVARFGITVTPTPLYSLSLVIIGVIGHVLVLVLIOHKKLRNWTSLYNL	77	:	:	:	:	:	:	:
Qy	85	AISDLLFLTLPWA-HSAAANEWFGNAMCKLFTGLYHIGFYGGIFFIILLTIDRYLAIV	143	:	:	:	:	:	:	:
Db	78	AISDLVFLSTLPFWVDYIMKGDWIFGNAMCFVSIFYVLGYSDMFFITLTIDRYLAVV	137	:	:	:	:	:	:	:
Qy	144	HAVPALKARTVTGVVTVSVITWLVAVFASVPGIIFTKCKEDSVVVCSPYPR----	199	:	:	:	:	:	:	:
Db	138	HWFALRARTVTFGIISSIIITWLAALSIPCLXYVFKSQMEFTHTCRAILFPRLIFL	197	:	:	:	:	:	:	:
Qy	200	NPHITMRNILGVLPLLTMVICSYGILATLCRNKKRHRAVRVIFTIMIYVFLFWTPY	259	:	:	:	:	:	:	:
Db	198	RFOALTWNILGLIPELLAMIICYTRIINVLR-RPNKKAKVMRLIFVITLFLFLLAPPY	256	:	:	:	:	:	:	:
Qy	260	NIVTLANTFOBFFGLSNCESTSQLDAQVTETLGMTGCCINPIIYAFVGKFRPYLSVF	319	:	:	:	:	:	:	:
Db	257	YLAAFVSAFEDVLFPPSCLRSQOVDLSLMITEALAYTHCCVNPVIVYVFGKRKYLWL	316	:	:	:	:	:	:	:
Qy	320	FRKHITKRFCKQCPVFBETVDGVTSTNTPSTGBQEVSAGL	360	:	:	:	:	:	:	:
Db	317	FRRHTAITLPOMLP-FLGEDRAORASARLPSTVELETADL	356	:	:	:	:	:	:	:

RESULT: 12  
JC5067  
G protein-coupled receptor CKR-L1 - human  
N:Alternate names: chemokine receptor-like protein TER1; GPR-CY6  
C:Species: Homo sapiens (man)  
C:Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #text\_change 09-Jul-2004  
C:Accession: JC5067; G02776; G02387  
R:Zaballos, A.; Varona, R.; Guierrez, J.; Lind, P.; Marquez, G.  
Biochem. Biophys. Res. Commun. 227, 846-853, 1996  
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like S  
A:Reference number: JC5067; MUID:97040707; PMID:8886020  
A:Accession: JC5067  
A:Molecule type: DNA  
A:Residues: 1-355 >ZAB>  
A:Cross-references: UNIPROT:P51685; EMBL:Z79782; NID:G1668735; PIDN:CAB02142.1; PID:G1668735  
R:Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: H01714  
A:Accession: G02776  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: DNA

A,Residues: 1-355 <NAP>  
A,Cross-references: EMBL:U62556; NID:gl468978; PID:gl468979  
R,Bonner, T.I.  
submitted to the EMBL Data Library, January 1996  
A,Reference number: H01154  
A,Accession: G02387  
A,Status: preliminary; translated from GB/EMBL/DBJ  
A,Molecule type: DNA  
A,Residues: 1-355 <BON>  
A,Cross-references: EMBL:U45983; NID:gl245056; PID:gl245057  
C,Comment: This protein belongs to the family of beta chemokine receptors.  
C,Genetics:  
A,Gene: GBP;CMKBR8; CMKBRL2; TERJ; CKR-L1  
A,Cross-references: GDB:6053733; OMIM:601834  
A,Map position: 3p21-3p21  
C,Superfamily: vertebrate rhodopsin  
C,Keywords: G protein-coupled receptor; transmembrane protein  
F,35-63/Domain: transmembrane #status predicted <TM>  
F,73-94/Domain: transmembrane #status predicted <TM>  
F,108-129/Domain: transmembrane #status predicted <TM3>  
F,147-171/Domain: transmembrane #status predicted <TM4>  
F,200-222/Domain: transmembrane #status predicted <TM5>  
F,239-260/Domain: transmembrane #status predicted <TM6>  
F,281-304/Domain: transmembrane #status predicted <TM7>

Query Match	39.5%;	Score 751;	DB 2;	Length 355;
Best Local Similarity	41.2%;	Pred. No. 2.6e-57;		
Matches	143;	Conservative 69;	Mismatches 121;	Indels 14; Gaps 5
Qy	20	VTTTFDDYD---CAPCHKPDVKIGAGLLPPLSLVPIFGVGNMLVLLINCKLKLC	75	
Db	9	VTTVTDDYYDPIDFSPCDABELIQNGKLLAVFCLLPVFSLLGNSLVILVLCVKLRS	68	
Qy	76	LTDYLLNLNLASDLLFLITLLPLWAHSRAANVWFGNAMCKLFTGLYHIGYFGGIFPILLT	135	
Db	69	ITDYLLNLNLASDLLFVSPFPQTYLLDQWVFGVMCKVSGFYIIGFYSSMFFITLMS	128	
Qy	136	IDRYLAIVHAFVAFKARTVTPGVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPFP	195	
Db	129	VDRYLAVVHAVYALKVRTIEMGTTCLCAWLTAIMATILPLVYFQVASEDVLQCYSPFN	188	
Qy	196	R---GWNNEFTIMENILGLVPLLIIMVICYSGILKTLIRCRNKKRRAVRVIFIMIVY	252	
Db	189	QQTALKWKIFTNFKWNILGELLPTTFIMFCYIKLHQLARQCNHKT-KAIRLVLIUVLAS	247	
Qy	253	FLFWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCINPIIYAFVGEKF	312	
Db	248	LLFWVPFNVVLPLASLSHMHILDGCSIQQLYATHVTEIISFTHCCVPNPIYAFVGEKF	307	
Qy	313	RRYLSVFRFKHITKRF---CKQCPVFRYRETVDGVTSTNTPSTGEQEV	356	
Db	308	KKHLSEIFOKSCSOFNYLGROMP---RESCEKSSSCQOHSSRSSSV	351	

RESULT 13

158186  
 probable G protein-coupled receptor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I58186  
 R:Harison, J.K.; Barber, C.M.; Lynch, K.R.  
 Neurosci. Lett. 169, 85-89, 1994  
 A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spin  
 A:Reference number: I58186, MUID:94323113, PMID:8047298  
 A:Accession: I58186  
 A>Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <RES>  
 A:Cross-references: UNIPROT:P35411; EMBL:U04808; NID:G2558635; PIDN:AAB8709  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G'protein-coupled receptor  
 Query Match 38.0%; Score 722.5; DB 2; Length 354;

[illegible]

```

126 DRYLAIVLAANSMNRRVTQHGVTISLGVAAAILVAAPQFMFTK-QKENE---CLGDYPE 181
197 GWNNFHTIMRNI-----LGLVPLLIIMVTCYSGILKTLRCNEKKHRAVRVIFTIMIV 252
182 VLQBIWPVLRNVEVNFGLPLLIIMSVCFRIQTFLSCKNHKA-KAIKLILLVVIIVF 240
253 FLFWTPYNNIVLLNTFQEFFGLSNCBSTSQLDQATQVTTGLMTHCCINPIIYAFVGEKF 312
241 FLFWTPYNNVIMFLETCLKLYDFPSPCDMRKDLRLALSVTETVAFSHCCINPLIYAFAGEKF 300
313 RRYLSVFRK 322
301 RRYLYHLYGK 310

RESULT 15
JC5942
Chemokine receptor - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: JC5942
E:Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 284-288, 1998
A:Title: Cloning and characterization of a novel human chemokine receptor.
A:Reference number: JC5942; MUID:98139902; PMID:9473515
A:Accession: JC5942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-344 <Fan>
A:Cross-references: UNIPROT:O00421; GB:U97123; NID:g2897070; PIDN:AAC39595.1;
C:Superfamily: vertebrate rhodopsin

Query Match 34.2%; Score 649.5; DB 2; Length 344;
Best Local Similarity 43.0%; Pred. No. 1.4e-48;
Matches 128; Conservative 54; Mismatches 99; Indels 17; Gaps 5

Qy 27 DYGAPECHKFDVKQIQAQLLPYLSLVFIFGVGNMLVLLILINCKKLKCLTDIYLLNLAI 86
Db 23 DEAEQCDKYDAQALSAQLVPSLCSAVFVIGVDNLVLVLLVYKGLKRVENIYLLNLAV 82
Qy 87 SDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVH-A 145
Db 83 SNLCFLTLPLFWAHAG-----GDPWCKILIGLYFVGLYSETFFNCLLTQVRYLVFLHKG 136
Qy 146 VPALKARTVFGVVTSVITMVAVFASVPGIIFTKCKEDSVYVCG-----PYFPRG--- 198
Db 137 NFFSARRRVPCGIITSLAWVTALITPEYVVYKPMQEDOKYKCAFSRTPELPADETFW 196
Qy 199 NNEHTIMRNLGLVPLLIIMVTCYSGILKTLRCNEKKHRAVRVIFTIMIVVFLFWTP 258
Db 197 KHEUTLQNNISVLPLPIFTFLYQWRKTU---RFQRYSFLKLVFAIMVVFLLMAP 253
Qy 259 YNIVILLNTFQEFFGLSNCBSTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRYL 316
Db 254 YNTAFFLSTPKHEFSLSDCKSSYNLDKSVHTIKLIATHTCCINPLIYAFLODTFFSKYL 311

Search completed: June 9, 2005, 16:49:04
Job time : 27.0136 secs

```

Search completed: June 9, 2005, 16:49:04  
Job time : 27.0136 secs

**THIS PAGE LEFT BLANK**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:28:38 ; Search time 111.335 Seconds  
(without alignments)  
1655.798 Million cell updates/sec

Title: US-10-791-166-4  
Perfect score: 1900  
Sequence: 1 MLSTSRSRFIRNTNBSREV.....DGVSTNTPSTGQEVSAQL 360

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	1845	97.1	1 CKR2_MACMU	O18793 macaca mla
2	1651.5	86.9	1 CKR2_HUMAN	P41597 homo sapien
3	1542	81.2	1 CKR2_RAT	O55193 rattus norv
4	1535	80.8	1 CKR2_MOUSE	P51683 mus musculu
5	1513	79.6	1 CKR2_MOUSE	Q6YT42 sus scrofa
6	1403	73.8	2 Q68G28	Q68G28 rattus norv
7	1396	73.5	1 CKR5_MOUSE	P51682 mus musculu
8	1392	73.3	2 Q95NC2	Q95NC2 callicebus
9	1386	72.9	1 CKR5_RAT	O08556 rattus norv
10	1383	72.8	2 Q6YT41	Q6YT41 sus scrofa
11	1377	72.5	2 Q6WN96	Q6WN96 leontopithe
12	1376	72.4	1 CKR5_CERTO	Q62743 cercocebus
13	1376	72.4	2 Q71RS2	Q71RS2 cercocebus
14	1375	72.4	2 Q8H2T9	Q8H2T9 saimiri sci
15	1375	72.4	2 Q9MZA0	Q9MZA0 callithrix
16	1375	72.4	2 Q6WN98	Q6WN98 callithrix
17	1374	72.3	2 Q95NE1	Q95NE1 cercocebus
18	1373	72.3	2 Q6WN93	Q6WN93 leontopithe
19	1373	72.3	2 Q6WN91	Q6WN91 leontopithe
20	1371	72.2	1 CKR5_HYLL	Q97883 hylobates l
21	1371	72.2	2 Q95NC4	Q95NC4 ateles geof
22	1371	72.2	2 Q95NC9	Q95NC9 alouatta se
23	1371	72.2	2 Q6WN97	Q6WN97 cebuella py
24	1371	72.2	2 Q9XT12	Q9XT12 cercoptithe
25	1370	72.1	1 CKR5_MACFA	P61814 macaca fasc
26	1370	72.1	1 CKR5_MACMU	P61813 macaca mla
27	1370	72.1	1 CKR5_MACNE	P61815 macaca neme
28	1370	72.1	1 CKR5_PANPA	P60574 pan paniscu
29	1370	72.1	1 CKR5_PANTR	P56440 pan troglod
30	1370	72.1	1 CKR5_PONPA	P61756 pongo pygma
31	1370	72.1	1 CKR5_PONPY	O97881 pongo pygma

32	1370	72.1	352	2	Q71TZ2	Q71TZ2 pongo pygma
33	1370	72.1	352	2	Q71TZ7	Q71TZ7 macaca nigr
34	1370	72.1	352	2	Q71TZ8	Q71TZ8 macaca tonk
35	1370	72.1	352	2	Q71TZ9	Q71TZ9 macaca sini
36	1368	72.0	352	1	CKR5_GORGO	P56439 gorilla gor
37	1368	72.0	352	1	CKR5_LOPAT	P61755 lophocebus
38	1368	72.0	352	1	CKR5_PAPAP	P68469 papio anubi
39	1368	72.0	352	1	CKR5_PAPHA	P68270 papio hamad
40	1368	72.0	352	2	O18770	O18770 pan troglod
41	1368	72.0	352	2	Q6WN92	Q6WN92 leontopithe
42	1368	72.0	352	2	Q6WN94	Q6WN94 leontopithe
43	1368	72.0	352	2	Q71TZ0	Q71TZ0 gorilla gor
44	1368	72.0	352	2	Q71TZ1	Q71TZ1 gorilla gor
45	1368	72.0	352	2	Q71UI8	Q71UI8 cercopithe

ALIGNMENTS

RESULT 1  
CKR2\_MACMU  
ID CKR2\_MACMU STANDARD; PRT; 360 AA.  
AC O18793;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 25-OCT-2004 (Rel. 45, Last annotation update)  
DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)  
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).  
GN Name=CCR2; Synonyms=CMKBR2;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=23354176; PubMed=11461684; DOI=10.1089/08922201750290104;  
RA Margulies B.J., Hauer D.A., Clements J.E.;  
RT "Identification and comparison of eleven rhesus macaque chemokine receptors."  
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
CC Transduces a signal by increasing the intracellular calcium ions level.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=B;  
CC IsoId=O18793-1; Sequence=Displayed;  
CC Name=A;  
CC IsoId=O18793-2; Sequence=Not described;  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  
EMBL; AF013958; AAD11572.1; -  
DR InterPro; IPR002237; CC 2 receptor.  
DR InterPro; IPR000355; ChmKine\_receptor.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1 1; 1.  
DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1 2; 1.  
KW Alternative splicing; G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.  
FT DOMAIN 1 42 Extracellular (Potential).  
FT TRANSMEM 43 70 1 (Potential).

FT	DOMAIN	71	80	Cytoplasmic (Potential).
FT	TRANSMEM	81	100	2 (Potential).
FT	DOMAIN	101	114	Extracellular (Potential).
FT	TRANSMEM	115	136	3 (Potential).
FT	DOMAIN	137	153	Cytoplasmic (Potential).
FT	TRANSMEM	154	178	4 (Potential).
FT	DOMAIN	179	206	Extracellular (Potential).
FT	TRANSMEM	207	226	5 (Potential).
FT	DOMAIN	227	243	Cytoplasmic (Potential).
FT	TRANSMEM	244	268	6 (Potential).
FT	DOMAIN	269	285	Extracellular (Potential).
FT	TRANSMEM	286	309	7 (Potential).
FT	DOMAIN	310	360	Cytoplasmic (Potential).
FT	CARBOHYD	14	14	N-linked (GlcNAc. .) (Potential).
FT	MOD RES	26	26	Sulfoxyrosine (By similarity).
FT	DISULFID	113	190	By similarity.
SQ	SEQUENCE	360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;		
Query Match				
Best Local Similarity 96.9%; Pred. No. 5.1e-106;				
Matches 349; Conservative 5; Mismatches 6; Indels 0; Gaps 0;				
QY	1	MLSTSRFIRNTNESGEVTF	FDYDYGAPCHKFDVKQIGQALLPPLYSLVFI	FGFVGN 60
DB	1	MLSTSRFIRNTNGSGEVT	TFDYDYGAPCHKFDVKQIGQALLPPLYSLVFI	FGFVGN 60
QY	61	MLVVLILNCKKGLCLDIYLLNLAISDLAFLTLPLWAHSAANEWF	FGNAMCKLFTGLY 120	
DB	61	MLVVLILNCKKGLSLDIYLLNLAISDLAFLTLPLWAHSAANEWF	FGNAMCKLFTGLY 120	
QY	121	HIGYFGGFIILLITIDRYLAIVHAFALKARTVFGVTSVITLWVAFASV	RGIIIFTK 180	
DB	121	HIGYLGIGFIILLITIDRYLAIVHAFALKARTVFGVTSVITLWVAFASV	PGIIFTK 180	
QY	181	CKEBSVYVCGPYFPRGWNFHTIMRNILGLVPLLIWICVSGILKTLRCNEKKRHR	240	
DB	181	COEEDSVYICGYPFPRGWNFHTIMRNILGLVPLLIWICVSGILKTLRCNEKKRHR	240	
QY	241	AVRVFTIMVYVFLFWTPNIVILLNTFOEFGLSNCSTSLDQATQV	TETLGMTHCCI 300	
DB	241	AVRLFTIMVYVFLFWTPNIVILLNTFOEFGLSNCSTSLDQATQV	TETLGMTHCCI 300	
QY	301	NPIIYAFVGEKFRRLYSVFRGHIITKRCKQCPVFRVVDGVTSTNP	STGEQVSVAGL 360	
DB	301	NPIIYAFVGEKFRRLYSVFRGHIITKRCKQCPVFRVVDGVTSTNP	STGEQVSVGL 360	
RESULT 2				
CKR2_HUMAN				
ID	CKR2	HUMAN	STANDARD;	PRT; 374 AA.
AC	P41597;			
DT	01-NOV-1995	(Rel. 32, Created)		
DT	01-NOV-1995	(Rel. 32, Last sequence update)		
DE	25-OCT-2004	(Rel. 45, Last annotation update)		
DE	C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)			
GN	(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).			
DE	Name=CCR2; Synonyms=CMKBR2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE=94195821; PubMed=8146186;			
RA	Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,			
RA	Coughlin S.R.;			
RT	"Molecular cloning and functional expression of two monocyte			
RT	chemoattractant protein 1 receptors reveals alternative splicing of			
RT	the carboxyl-terminal tails."			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=94324942; PubMed=8048929;			

RA	Yanagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;			
RT	"cDNA cloning and functional expression of a human monocyte			
RT	chemoattractant protein 1 receptor."			
RL	Biochem. Biophys. Res. Commun. 202:1156-1162(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;			
RA	Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;			
RT	"Organization and differential expression of the human monocyte			
RT	chemoattractant protein 1 receptor gene. Evidence for the role of the			
RT	carboxyl-terminal tail in receptor trafficking."			
RN	J. Biol. Chem. 272:1038-1045(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,			
RA	Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,			
RA	Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,			
RA	Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,			
RA	Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,			
RA	Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,			
RA	Sagranti J.B.;			
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.			
RA	Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,			
RA	Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;			
RT	"SeattlesNPs. NHLBI HL66682 program for genomic applications, UW-			
RT	FKRC, Seattle, WA (URL: <a href="http://pga.gs.washington.edu">http://pga.gs.washington.edu</a> ).";			
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SULFATION OF TYR-26, AND N-GLYCOSYLATION.			
RX	MEDLINE=20501139; PubMed=11046064;			
RA	Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,			
RA	Chakravarty L., Kolattukudy P.E.;			
RT	"Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that			
RT	has tyrosine sulfation in a conserved extracellular N-terminal			
RT	region."			
RL	J. Immunol. 165:5295-5303(2000).			
CC	-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.			
CC	Transduces a signal by increasing the intracellular calcium ions			
CC	level. Alternative coreceptor with CD4 for HIV-1 infection.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- ALTERNATIVE PRODUCTS:			
CC	Event-Alternative splicing; Named isoforms=2;			
CC	Name=A;			
CC	Isoid=P41597-1; Sequence=Displayed;			
CC	Name=B;			
CC	Isoid=P41597-2; Sequence=VSP_001893;			
CC	-!- PTM: N-glycosylated.			
CC	-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; U03882; AAA19119.1; -			
DR	EMBL; U03905; AAA19120.1; -			
DR	EMBL; D29984; BAA06253.1; -			
DR	EMBL; U80924; AAC51637.1; -			
DR	EMBL; U80924; AAC51636.1; -			
DR	EMBL; U95626; AAB57791.1; -			
DR	EMBL; U95626; AAB57792.1; -			
DR	EMBL; AF545480; AAN16400.1; -			
DR	PIR; I38450; I38450.			
DR	PIR; JC2443; JC2443.			
DR	PDB; 1KAD; Model; A=1-349.			
DR	PDB; 1KPI; Model; A=1-349.			
DR	Genew; HGNC:1603; CCR2.			
DR	MIM; 601267; -.			

DR GO: 0005887; C-integral to plasma membrane; TAS.  
 DR GO: 0005625; C-soluble fraction; TAS.  
 DR GO: 0004950; F-chemokine receptor activity; TAS.  
 DR GO: 00019735; P-antimicrobial humoral response (sensu Verte. . . ; TAS.  
 DR GO: 0006968; P-cellular defense response; TAS.  
 DR GO: 0006935; P-chemotaxis; TAS.  
 DR GO: 0007204; P-cytosolic calcium ion concentration elevation; TAS.  
 DR GO: 0006954; P-inflammatory response; TAS.  
 DR GO: 0007259; P-JAK-STAT cascade; TAS.  
 DR GO: 0007194; P-negative regulation of adenylate cyclase ac. . . ; TAS.  
 DR InterPro: IPR002237; CC 2 receptor.  
 DR InterPro: IPR000355; Chkline receptor.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE: PS0262; G-PROTEIN RECEPTOR FL2; 1.  
 DR 3D-structure: Alternative splicing; G-protein coupled receptor;  
 KW Glycoprotein; Polymorphism; Sulfation; Transmembrane;  
 FT DOMAIN 1 42 Extracellular (Potential).  
 FT TRANSMEM 43 70 1 (Potential).  
 FT DOMAIN 71 80 Cytoplasmic (Potential).  
 FT TRANSMEM 81 100 2 (Potential).  
 FT DOMAIN 101 114 Extracellular (Potential).  
 FT TRANSMEM 115 136 3 (Potential).  
 FT DOMAIN 137 153 Cytoplasmic (Potential).  
 FT TRANSMEM 154 178 4 (Potential).  
 FT DOMAIN 179 206 Extracellular (Potential).  
 FT TRANSMEM 207 226 5 (Potential).  
 FT DOMAIN 227 243 Cytoplasmic (Potential).  
 FT TRANSMEM 244 268 6 (Potential).  
 FT DOMAIN 269 285 Extracellular (Potential).  
 FT TRANSMEM 286 309 7 (Potential).  
 FT DOMAIN 310 374 Cytoplasmic (Potential).  
 FT CARBOHYD 14 14 N-linked (GlcNAc. . . ) (Potential).  
 FT MOD RES 26 26 Sulfotyrosine.  
 FT DISULFID 113 190 By similarity.  
 FT VARSPLIC 314 374 isoform B).  
 FT VARIANT 64 64 /FTID=VSP\_001893.  
 FT VARIANT 355 355 V -> I (in dbSNP:1799864).  
 FT VARIANT 355 355 /FTID=VAR\_014339.  
 FT SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;  
 Query Match 86.9%; Score 1651.5; DB 1; Length 374;  
 Best Local Similarity 95.5%; Pred. No. 4.2e-94;  
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;  
 QY 1 MLSTSRSPRINTNSESBEVTFPPDYDYGAPCHKEFDVQKIGQALLPPLYSLVFIQFVGN 60  
 DB 1 MLSTSRSPRINTNSESBEVTFPPDYDYGAPCHKEFDVQKIGQALLPPLYSLVFIQFVGN 60  
 QY 61 MLVLLINCKKLCITDIYLLNLAIISDLLFTILPLWAHSAANEVFGNACKLFTGLY 120  
 DB 61 MLVLLINCKKLCITDIYLLNLAIISDLLFTILPLWAHSAANEVFGNACKLFTGLY 120  
 QY 121 HIGYGGFFILLTIDRYLAIVHAFKARTVTFGVVTSVITLWVAFVSPGIIPTK 180  
 DB 121 HIGYGGFFILLTIDRYLAIVHAFKARTVTFGVVTSVITLWVAFVSPGIIPTK 180  
 QY 181 COKEDSVVCGPYPRGWNHETMRNIGLVPLIMVICYSGILKTLACRNEKKHR 240  
 DB 181 COKEDSVVCGPYPRGWNHETMRNIGLVPLIMVICYSGILKTLACRNEKKHR 240  
 QY 241 AVRVLFTIMVFLFTWPNIVILLNTFOEPGLSNCSTSLDQATQVETLGMHCCI 300  
 DB 241 AVRVLFTIMVFLFTWPNIVILLNTFOEPGLSNCSTSLDQATQVETLGMHCCI 300  
 QY 301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPV 334

DB 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327  
 ||||| ||||| ||: || ||: ||:  
 RESULT 3  
 CCR2\_RAT  
 ID CCR2\_RAT STANDARD; PRT; 373 AA.  
 AC O55193;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-C CCR-2) (CCR-2) (CCR2).  
 GN Name=CCR2; Synonyms=Cckbr2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=98318173; PubMed=9655467; DOI=10.1016/S0165-5728(98)00005-8;  
 RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
 RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
 RT "Chemokine receptor expression in cultured glia and rat experimental  
 RT allergic encephalomyelitis";  
 RL J. Neuroimmunol. 86:1-12(1998).  
 CC -!- FUNCTION: Receptor for the MCP-1 (J.E), MCP-3 (FIC) and MCP-5  
 CC chemokines. Transduces a signal by increasing the intracellular  
 CC calcium ions level (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and  
 CC macrophages.  
 CC -!- INDUCTION: In animals in which experimental allergic  
 CC encephalomyelitis (EAE) has been induced.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC  
 CC EMBL: U77349; AAC03242.1; -.  
 DR RGD: 620876; Ccr2.  
 DR InterPro: IPR002237; CC 2 receptor.  
 DR InterPro: IPR000355; Chkline\_receptor.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE: PS0262; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 60 Extracellular (Potential).  
 FT TRANSMEM 61 81 Potentia.  
 FT DOMAIN 82 91 Cytoplasmic (Potential).  
 FT TRANSMEM 92 112 Potentia.  
 FT DOMAIN 113 128 Extracellular (Potential).  
 FT TRANSMEM 129 149 Potentia.  
 FT DOMAIN 150 170 Cytoplasmic (Potential).  
 FT TRANSMEM 171 191 Potentia.  
 FT DOMAIN 192 220 Extracellular (Potential).  
 FT TRANSMEM 221 241 Potentia.  
 FT DOMAIN 242 256 Cytoplasmic (Potential).  
 FT TRANSMEM 257 277 Potentia.  
 FT DOMAIN 278 301 Extracellular (Potential).  
 FT TRANSMEM 302 322 Potentia.  
 FT DOMAIN 323 373 Cytoplasmic (Potential).  
 FT DISULFID 126 203 By similarity.  
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;  
 Query Match 81.2%; Score 1542; DB 1; Length 373;

Best Local Similarity 80.0%; Pred. No. 2.3e-87;  
Matches 288; Conservative 24; Mismatches 48; Indels 0; Gaps 0;

QY 1 MLSTSRFRINTWESGEEVTFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIQFVGN 60  
DB 14 ILTSHSLFTRSIQELDEGATTPYDDGEPCHKTSVKQIGAWILPPLYSLVFIQFVGN 73  
QY 61 MLVVLILNCKKLCITDIYLLNLAISDLLFLTLPLWAHSAANEVFGNACKLFTGLY 120  
DB 74 MLVVLILNCKKLSMTDIYLLNLAISDLLFLTLPLWAHSAANEVFGNACKLFTGLY 133  
QY 121 HIGYFGGIFILLTIDRYLAIVHAFKARTTFFGVVTSVITLWVAFASVPGIIFTK 180  
DB 134 HIGYFGGIFILLTIDRYLAIVHAFKARTTFFGVVTSVITLWVAFASVPGIIFTK 193  
QY 181 COKEDSVVVCYPPRGNNFHTIMRNILGLVPLILNIVICYSGLIKTLRCRNEKKRHR 240  
DB 194 SEQEDDQHTCGPYPTIMKNFQTIMRNILSILPLVNVICYSGLIKTLRCRNEKKRHR 253  
QY 241 AVRVFTIMVYFLFWTPYINIVILNTPQEFGLSNCESTSQLDQATQVETLGMTHCCI 300  
DB 254 AVRLIFALMIVYFLFWTPYINIVILNTPQEFGLSNCESTSQLDQATQVETLGMTHCCI 313  
QY 301 NPITVAFGKFRYLSVFFPKHITRCKOCPPYRETVDGVTSTNTPSTGGEQVSAGL 360  
DB 314 NPITVAFGKFRYLSVFFPKHITRCKOCPPYRETVDGVTSTNTPSTGGEQVSAGL 373

RESULT 4  
ID\_CKR2 MOUSE STANDARD; PRT; 373 AA.

AC P51683; O61172;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2)  
DE (JE/FIC receptor) (MCP-1 receptor).  
GN Name=Ccr2; Synonyms=Cmkbr2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;  
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,  
RA Charo I.F.;  
RA "Molecular cloning and functional expression of murine JE (monocyte  
chemoattractant protein 1) and murine macrophage inflammatory protein  
1 alpha receptors: evidence for two closely linked C-C chemokine  
receptors on chromosome 9.";  
RL J. Biol. Chem. 271:7551-7558 (1996).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=BALB/C;  
RX MEDLINE=96216064; PubMed=8662823; DOI=10.1074/jbc.271.20.11603;  
RA Kurihara T., Bravo R.;  
RA "Cloning and functional expression of mCCR2, a murine receptor for the  
C-C chemokines JE and FIC.";  
RL J. Biol. Chem. 271:11603-11606 (1996).  
RN [3]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=97026720; PubMed=8872898;  
RX DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNMR73.3.CO;2-H;  
RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,  
RA Post T.W., Gerard C., Dorf M.E.;  
RA "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse  
transcriptase-polymerase chain reaction does not detect mRNA for the  
KC or new MCP-1 receptor.";  
RL J. Neurosci. Res. 45:382-391 (1996).  
CC -/- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5  
chemokines. Transduces a signal by increasing the intracellular  
calcium ions level.

-/- SUBCELLULAR LOCATION: Integral membrane protein.  
-/- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,  
but not in nonhematopoietic cell lines.  
-/- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
-----  
DR EMBL; U47035; AAC52453.1; -;  
DR EMBL; U58119; AAC52557.1; -;  
DR EMBL; U56819; AAC52784.1; -;  
DR MGD; MGI:106185; Ccr2.  
DR GO; GO:0016493; P:C-C chemokine receptor activity; IDA.  
DR GO; GO:0019955; P:cytokine binding; IPI.  
DR GO; GO:0016086; P:cellular defense response (sensu Vertebrata); IMP.  
DR GO; GO:0030097; P:hemoopoiesis; IMP.  
DR GO; GO:0006959; P:humoral immune response; IMP.  
DR GO; GO:0006954; P:inflammatory response; IMP.  
DR GO; GO:0019233; P:perception of pain; IMP.  
DR GO; GO:0030334; P:regulation of cell migration; IMP.  
DR InterPro; IPR002237; CC\_2\_receptor.  
DR InterPro; IPR000355; Cmkine\_receptor.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHOPOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
DR G-protein coupled receptor; Transmembrane.  
KW DOMAIN 1 55 Extracellular (Potential).  
FT TRANSMEM 56 83 1 (Potential).  
FT DOMAIN 84 93 Cytoplasmic (Potential).  
FT TRANSMEM 94 114 2 (Potential).  
FT DOMAIN 115 127 Extracellular (Potential).  
FT TRANSMEM 128 149 3 (Potential).  
FT DOMAIN 150 166 Cytoplasmic (Potential).  
FT TRANSMEM 167 191 4 (Potential).  
FT DOMAIN 192 219 Extracellular (Potential).  
FT TRANSMEM 220 239 5 (Potential).  
FT DOMAIN 240 256 Cytoplasmic (Potential).  
FT TRANSMEM 257 281 6 (Potential).  
FT DOMAIN 282 298 Extracellular (Potential).  
FT TRANSMEM 299 322 7 (Potential).  
FT DOMAIN 323 373 Cytoplasmic (Potential).  
FT DISULFID 126 203 By similarity.  
FT CONFLICT 39 39 Y -> H (in Ref. 1).  
FT CONFLICT 184 184 A -> G (in Ref. 1).  
FT CONFLICT 264 264 V -> G (in Ref. 1).  
SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;  
Query Match 80.8%; Score 1535; DB 1; Length 373;  
Best Local Similarity 79.7%; Pred. No. 6.1e-87;  
Matches 287; Conservative 25; Mismatches 48; Indels 0; Gaps 0;

QY 1 MLSTSRFRINTWESGEEVTFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIQFVGN 60  
DB 14 ILTSHSLFTRSIQELDEGATTPYDDGEPCHKTSVKQIGAWILPPLYSLVFIQFVGN 73  
QY 61 MLVVLILNCKKLCITDIYLLNLAISDLLFLTLPLWAHSAANEVFGNACKLFTGLY 120  
DB 74 MLVVLILNCKKLSMTDIYLLNLAISDLLFLTLPLWAHSAANEVFGNACKLFTGLY 133  
QY 121 HIGYFGGIFILLTIDRYLAIVHAFKARTTFFGVVTSVITLWVAFASVPGIIFTK 180  
DB 134 HIGYFGGIFILLTIDRYLAIVHAFKARTTFFGVVTSVITLWVAFASVPGIIFTK 193  
QY 181 COKEDSVVVCYPPRGNNFHTIMRNILGLVPLILNIVICYSGLIKTLRCRNEKKRHR 240  
DB 194 SKQDDHHYTCGPFYFQLMKNFQTIMRNILSILPLVNVICYSGLIKTLRCRNEKKRHR 253



```

QY 241 AVRVIETIMIVFLFWTPYINIVILLNTFQBFGLSNCSTSSQLDQATQVTTETLGMTHCCI 300
DB 254 AVRLIFAIMTIVYFLFWTPYINIVLFTTQBSLGMSCNVCIDKHLDDQAMQVTTETLGMTHCCI 313
QY 301 NPIIYAFVGEKFRYLSVFFRKHITKRCFKQCPVFYRETVDGVTSTNTSTGQEQVSAGL 360
DB 314 NPVIYAFVGEKFRYLSVFFRKHIAKRLCKQCPVFYRETADRVSTTPTSTGQEQVSAGL 373

RESULT 5
Q6YT42 PRELIMINARY; PRT; 373 AA.
ID O6YT42
AC O6YT42; 27, Created
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 2 (Chemokine C-C motif receptor
DE 2).
GN Name=CCR2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
RA Uenishi H.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006185; BAD08648.1; -.
DR EMBL; AP006435; BAD08655.1; -.
DR EMBL; AB119271; BAD12134.1; -.
DR GO; GO:0016021; C.integral to membrane; IEA.
DR GO; GO:0016493; R-C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR GO; GO:0001584; F-rihodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P-G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR002237; CC 2 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR Pfam; PF00001; 7tm1_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01107; CHEMOKINER2.
DR PROSITE; PS00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G-PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 373 AA; 42299 MW; FAE55CA527A34E0 CRC64;

Query Match
Best Local Similarity 79.6%; Score 1513; DB 2; Length 373;
Matches 284; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

QY 1 MUGSRFIRNTNSGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN 60
DB 14 VLPTSHSLTWNKGNDEBPTTSYDYDSEPCQKTSVGQIEALLPPLYSLVFIFFGVGN 73
QY 61 MNAVLLINCKKLCITDIYILNLAISDLLFLITPLWHAASANEVFNAGMKLFTGLY 120
DB 74 LLWVLLINCKKLGKNTDIYILNLAISDLLFLITPFWAHYAADQWVFNCKEFTGLY 133
QY 121 HGYFGGIFPILLITDRLAIVHAFALKARTVFGVVTSTVITWLVAFASVPGIIFTK 180
DB 134 HGYFGGIFPILLITDRLAIVHAFALKARTVFGVVTSTVITWLVAFASVPGIIFIR 193

```

```

QY 181 CQKEDSVYVCGPYFPRGWNNTHTMNIILGLVLPLIMVICYSGILKTLRCNEKKRHR 240
DB 194 SOBESGYACAPYFPLAWKNTHTMNIILGLVLPLIMVICYSGILKTLRCNEKKRHR 253
QY 241 AVRVIETIMIVFLFWTPYINIVILLNTFQBFGLSNCSTSSQLDQATQVTTETLGMTHCCI 300
DB 254 AVRLIFAIMTIVYFLFWTPYINIVLFTTQBSLGMSCNVCIDKHLDDQAMQVTTETLGMTHCCI 313
QY 301 NPIIYAFVGEKFRYLSVFFRKHITKRCFKQCPVFYRETVDGVTSTNTSTGQEQVSAGL 360
DB 314 NPVIYAFVGEKFRYLSVFFRKHIAKRLCKQCPVFYRETADRVSTTPTSTGQEQVSAGL 373

RESULT 6
Q68G28 PRELIMINARY; PRT; 354 AA.
ID O68G28
AC O68G28; 28, Created
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Chemokine (C-C) receptor 5.
GN Name=Cmbbr5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Tissue-Kidney.
RC Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC078756; AAH78756.1; -.
DR GO; GO:0004872; F-receptor activity; IEA.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chkline_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00196; COPPER BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G-PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 354 AA; 41081 MW; 4CCB9A9C4EE985C CRC64;

Query Match
Best Local Similarity 73.8%; Score 1403; DB 2; Length 354;
Matches 284; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

```

Matches		264;	Conservative	30;	Mismatches	50;	Indels	6;	Gaps	2;
Qy	17	GEEVTTTFDYD--GAPCHKFDVKQIGAGLLPPLYSLVFPGFVGNMLVWLILNCKKX 74								
Db	5	GSIPTIYIDYSAPCKENKVAIAQLPPLYSLVFPGFVGNMVFLLISCKKX 64								
Qy	75	CLTDIYLNLAIISLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHIGYGGIFPILL 134								
Db	65	SMTDIYLFNLAIISLLFLITLPLFARHAAANWVFGNINCKLFTGIYHIGYGGIFPILL 124								
Qy	135	TIDRYLAIVHAFKARTVTFGVVTSVITLWVAFAVSVPGLIIFTKQKEDSVVVCOPYF 194								
Db	125	TIDRYLAIVHAFKARTVTFGVVTSVITLWVAFAVSVPGLIIFTKQKEDSVVVCOPYF 184								
Qy	195	P----RGWNNFHTIMRNILGVLPLIMVICYSGLIKTLRCNEKKRRAVRVIFTIMI 250								
Db	185	PRIQRFWKHFQTLKWVLSLILPLVWVICYSGILNTLPCRNEKKRRAVRILPAIMI 244								
Qy	251	VYFLFWTPYNTVILNTQBFGLSNCESTSQLDOATQVTTGLMTHCCINPIIYAFVGE 310								
Db	245	VYFLFWTPYNTVILNTQBFGLSNCESTSQLDOATQVTTGLMTHCCINPIIYAFVGE 304								
Qy	311	KFRYLSVFFKHTKCKCPYRETVDGVTSTNTPSGEORVSAGL 360								
Db	305	KFRYLSVFFKHTKCKCPYRETVDGVTSTNTPSGEORVSAGL 354								

RESULT 7

CKR5\_MOUSE STANDARD; PRT: 354 AA.

ID AC CKR5\_MOUSE STANDARD; PRT: 354 AA.

AD P51682; O35313; O35891; P97308; P97405; Q61867;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR-5) (MIP-1 alpha receptor).

GN Name=Ccr5; Synonyms=Cmkbr5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvJ; TISSUE=Spleen;

RX MEDLINE=96205938; PubMed=86311787; DOI=10.1074/jbc.271.13.7551;

RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L., Charo I.F.; Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein 1 alpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.

RL J. Biol. Chem. 271:7551-7558 (1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;

RX MEDLINE=96278910; PubMed=8662890; DOI=10.1074/jbc.271.24.14445;

RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.; "Cloning and characterization of a novel murine macrophage inflammatory protein-1 alpha receptor."

RL J. Biol. Chem. 271:14445-14451 (1996).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/Ola;

RX Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;

RX MEDLINE=98001387; PubMed=9343222;

RA Kuhnmann S.E., Platt E.J., Korak S.L., Kabat D.;

RT "Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses."

J. Virol. 71:8642-8656 (1997).

[5]

SEQUENCE FROM N.A.

RC STRAIN=129;

RX MEDLINE=97404635; PubMed=9261347;

RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H., Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.; "Two distinct CCR5 domains can mediate coreceptor usage by human immunodeficiency virus type 1."

RT J. Virol. 71:6305-6314 (1997).

RN [6]

SEQUENCE FROM N.A.

RC Guo B., Kuno K., Harada A., Matsuhashima K.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.

CC -I- SUBCELLULAR LOCATION: Integral membrane protein.

CC -I- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines, but not in nonhematopoietic cell lines.

CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----

CC EMBL: U47036; AAC52454.1; -

CC EMBL: X94151; CA63867.1; -

CC EMBL: U68565; AAB37273.1; -

CC EMBL: U83327; AAC53386.1; -

CC EMBL: AF022990; AAC53389.1; -

CC EMBL: AF019772; AAB71183.1; -

CC EMBL: D83648; BAA12024.1; -

CC MGD: MG1:107182; Ccr5.

CC GO: GO:0016493; F:C-C chemokine receptor activity; IDA.

CC GO: GO:0006952; P:defense response; IMP.

CC InterPro: IPR002240; CC 5 receptor.

CC InterPro: IPR003355; Chkline receptor.

CC InterPro: IPR000276; GPCR\_Rhodpsn.

CC Pfam: PF00001; 7tm.1; 1.

CC PRINTS: PR00237; GPCR\_Rhodopsin.

DR	PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR	PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
DR	G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
FT	DOMAIN 1 32 Extracellular (Potential).
FT	TRANSMEM 33 60 1 (Potential).
FT	DOMAIN 61 70 Cytoplasmic (Potential).
FT	TRANSMEM 71 91 2 (Potential).
FT	DOMAIN 92 104 Extracellular (Potential).
FT	TRANSMEM 105 126 3 (Potential).
FT	DOMAIN 127 143 Cytoplasmic (Potential).
FT	TRANSMEM 144 168 4 (Potential).
FT	DOMAIN 169 200 Extracellular (Potential).
FT	TRANSMEM 201 220 5 (Potential).
FT	DOMAIN 221 237 Cytoplasmic (Potential).
FT	TRANSMEM 238 262 6 (Potential).
FT	DOMAIN 263 279 Extracellular (Potential).
FT	TRANSMEM 280 303 7 (Potential).
FT	DOMAIN 304 354 Cytoplasmic (Potential).
FT	DISEASE: 103 By similarity.
FT	CARBOHYD 270 270 N-linked (GlcNAc...) (Potential).
FT	VARIANT 11 11 I -> S.
FT	VARIANT 66 66 K -> R.
FT	VARIANT 66 66 V -> M.
FT	VARIANT 97 97 I -> V.
FT	VARIANT 109 109 V -> L.
FT	VARIANT 156 156 V -> A.
FT	VARIANT 160 160 P -> S.
FT	VARIANT 185 185 P -> L.

DR		PROSITE; PS00196;	COPPER BLUE; UNKNOWN 1.
DR		PROSITE; PS0237;	G PROTEIN RECF FL 1; 1.
DR		PROSITE; PS0262;	G PROTEIN RECF FL 2; 1.
KW		G-protein coupled receptor; Receptor; Transmembrane.	
SQ		SEQUENCE	352 AA; 40495 MW; 7FB307513ACF89B CRC64;
 Query Match                  73.3%; Score 1392; DB 2; Length 352; Best local similarity        75.4%; Pred.No. 3.6e-78; Matches 263; Conservative 30; Mismatches 50; Indels 6; Gaps 2;			
Yq	18	EVTTFDYDGA--PCHKFDVKIQAGLLPPILYSLVFTFGVGNMLVLILNCKKLKC	75
Dd	4	EVSPDIIDYGASEPCQKDINKOMQAQLLPLIYSVMVLFVGFGNNMLWLILNCRLKS	63
Yq	76	LTDYLNLALISDLLFLITLPLWAHSAANEWFENAMCKLFTGLXHGIVGGFFFIILLT	135
Dd	64	MTHLYLNLAISDLFPFLTVPFWAHVAAGWDGTMCQPLTGSLYFIGFSGIFFIIILT	123
Yq	136	IDRYLIAIHAVAFALKARTVTFGVTVITWLVAVFAASPGVIIFTKOKEDSVVVCGPYPF	195
Dd	124	IDRYLIAIHAVAFALKARTVTFGVTVITWWVAVPASLPGLIIFTRSOKEYHYTCSPHPF	183
Yq	196	RG-----WNPHHTMRNILGHVTLPLLHWICSYGIILATLCRNEKKRHRAVRVFIMIV	251
Dd	184	FQGRFMKNLETLKWIVLGVLPLVNVVICSYGIILKTLLCRNEKKRRHAVRLFIMIV	243
Yq	252	YFLFWTPYNIVLIINTFOBFGLSNCESTSOLDQATQTETLTGMTCCNPPIIAFVGEK	311
Dd	244	YFLWPAYNIIVLIINTYQBFGLNCSNRLEDQANOVLETIGMTHCVCNPPIIAFVGEK	303
Yq	312	FRRLSVPRFKHITHRKFCQCQPYYRETVDGVSTNTPTSGEVSAGL	360
Dd	304	FRNYLLVFFOKHAKRFKCCSIFQEAPERANSVYTSTRSGEQEISVGL	352
 RESULT 9 CKR5 RAT      STANDARD; PRT; 354 AA. AC AC O08556; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 25-OCT-2004 (Rel. 45, Last annotation update) DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1 alpha receptor). DE Names=Ccr5; Synonyms=cmkr5; OS Rattus norvegicus (Rat). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus. OX NCBI_TaxID=10116; RN RN [1] RP SEQUENCE FROM N.A. RC STRAIN=Wistar; TISSUE=Brain; RX MEDLINE=98334084; PubMed=9670989; RX DOI=10.1002/(SICI)1097-4547(19980701)53:1<16:AID-JNR3>3.3.CO;2-D; RA Spleiss O., Gourmalan N., Boddeke H.W.G.M., Sauter A., Fiebich B.L., Berger M., Gebicke-Haertel P.J.; RT "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and upregulation of its mRNA in ischemic and endotoxinemic rat brain."; RT J. Neurosci. Res. 53:16-28(1998). RN RN [2] RP SEQUENCE FROM N.A. RC STRAIN=Sprague-Dawley; RX MEDLINE=98318173; PubMed=9655467; DOI=10.1016/S0165-5728(98)00005-8; RA Jiang Y., Salafraanca M.N., Adhkari S., Xia Y., Feng L., Sonntag M.K., Defibere C.M., Pennell N.A., Streit W.J., Harrison J.K.; RT "Chemokine receptor expression in cultured glial and rat experimental allergic encephalomyelitis". RT J. Neurolimmunol. 86:1-12(1998). CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, CC MIP-1-beta and RANTES and subsequently transduces a signal by CC increasing the intracellular calcium ions level. CC -II- SUBCELLULAR LOCATION: Integral membrane protein. CC CC -III SIMILARITY: Belongs to the G-protein coupled receptor 1 family.			

-----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----

EMBL; Y12009; CAA72737.1; -;  
 EMBL; U77350; AAC03243.1; -;  
 RGD; 620596; Cmkbr5.  
 InterPro; IPR002240; CC\_5\_receptor.  
 InterPro; IPR000355; Chkline\_receptor.  
 InterPro; IPR000276; GPCR\_Rhodpsn.  
 Pfam; PF00001; 7tm 1; 1.  
 PRINTS; PR00237; GPCRHHODPSN.  
 PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 G-protein coupled receptor; Glycoprotein; Transmembrane.  
 FT DOMAIN 1 32 Extracellular (Potential).  
 TRANSMEM 33 60 1 (Potential).  
 DOMAIN 61 70 2 (Potential).  
 TRANSMEM 71 91 2 (Potential).  
 DOMAIN 92 104 3 (Potential).  
 TRANSMEM 105 126 3 (Potential).  
 DOMAIN 127 143 Cytoplasmic (Potential).  
 TRANSMEM 144 168 4 (Potential).  
 DOMAIN 169 200 Extracellular (Potential).  
 TRANSMEM 201 220 5 (Potential).  
 DOMAIN 221 237 Cytoplasmic (Potential).  
 TRANSMEM 238 262 6 (Potential).  
 DOMAIN 263 279 Extracellular (Potential).  
 TRANSMEM 280 303 7 (Potential).  
 DOMAIN 304 354 Cytoplasmic (Potential).  
 DISULFID 103 180 By similarity.  
 CARBOHYD 270 270 N-linked (GlcNAc..). (Potential).  
 SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 72.9%; Score 1386; DB 1; Length 354;  
 Best Local Similarity 74.9%; Pred. No. 8.5e-78;  
 Matches 262; Conservative 30; Mismatches 52; Indels 6; Gaps 2;  
 QY 17 GSEVTFDDYD--GAPCHKFDVKGQIAGQLLPPLYSLVIFGFGVGNMLVLLINCKK 74  
 Db 5 GSIPYIVYDIDYMSGAPCKQVNVKQIAQLLPPLYSLVIFGFGVGNMVFLLISCKK 64  
 QY 75 CLTDIYLLNLAISDLFLTLPLWAHSAANEVFGNMLKFTGLYHIGYFGGIFILL 134  
 Db 65 SMTDIYLFNLAISDLFLTLPLWAHSAANEVFGNIMCKLFTGIYHIGYFGGIFILL 124  
 QY 135 TIDRYLAIHVAHPALKARTVTFGVTSVITLVAVPASVPGIIFTCKQEDSVYVCGPYF 194  
 Db 125 TIDRYLAIHVAHPALKARTVTFGVTSVITLVAVPASVPGIIFTCKQEDSVYVCGPYF 184  
 QY 195 -----PRGNNFHTMNIILGLVPLIMVICYSGILKTLRLCRNEKKHRAVRVFTIMI 250  
 Db 185 LHIQYRFKWHFQTLKMWLSLILPLLMVICYSGILNTLFRCKNEKKHRAVRLIFAIMI 244  
 QY 251 VYFLFWTPYNIIVLLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGE 310  
 Db 245 VYFLFWTPYNIIVLLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGE 304  
 QY 311 KFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPTSTGQEVSA 360  
 Db 305 KFRYLSVFRKHIVKRFCKHSIFQVNPDRVSSVYVTRSTGQEVSTGL 354  
 RESULT 10  
 ID Q6YT41 PRELIMINARY; PRT; 352 AA.  
 AC Q6YT41;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Chemokine (C-C motif) receptor 5 (Chemokine C-C motif eceptor 5).  
 GN Name=CCRS;  
 OS Sus scrofa (pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,  
 Uenishi H.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AP006185; BAD08649.1; -;  
 DR EMBL; AP006435; BAD08656.1; -;  
 DR EMBL; AB119272; BAD12135.1; -;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro; IPR000923; BlueCu.1.  
 DR InterPro; IPR002240; CC\_5\_receptor.  
 DR InterPro; IPR000355; Chkline\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00657; CCHEMOKINER.  
 DR PRINTS; PR01110; CHEMOKINERS.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00196; COPPER BLUE; UNKNOWN\_1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 352 AA; 40227 MW; 7464CB930911C987 CRC64;  
 Query Match 72.8%; Score 1383; DB 2; Length 352;  
 Best Local Similarity 74.5%; Pred. No. 1.3e-77;  
 Matches 260; Conservative 33; Mismatches 50; Indels 6; Gaps 2;  
 QY 18 EVVTFDDYDYG--APCHKFDVKGQIAGQLLPPLYSLVIFGFGVGNMLVLLINCKK 75  
 Db 4 QTSFPYDIDYMSGPECKTNRQIAARLLPPLYSLVIFGFGVGNMLVLLINCKK 63  
 QY 76 LTDIYLLNLAISDLFLTLPLWAHSAANEVFGNMLKFTGLYHIGYFGGIFILL 135  
 Db 64 MTDIYLLNLAISDLFLTLPLWAHSAANEVFGNMQFLTGFGYFGGIFILL 123  
 QY 136 IDRYLAIHVAHPALKARTVTFGVTSVITLVAVPASVPGIIFTCKQEDSVYVCGPYF 195  
 Db 124 IDRYLAIHVAHPALKARTVTFGVTSVITLVAVPASVPGIIFTCKQEDSVYVCGPYF 183  
 QY 196 RG-----WNFHTMNIILGLVPLIMVICYSGILKTLRLCRNEKKHRAVRVFTIMI 251  
 Db 184 SSQYHFKNFQTLKMWLSLILPLLMVICYSGILKTLRLCRNEKKHRAVRVFTIMI 243  
 QY 252 YFLFWTPYNIIVLLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGE 311  
 Db 244 YFLFWTPYNIIVLLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGE 303  
 QY 312 KFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPTSTGQEVSA 360  
 Db 304 KFRYLSVFRKHIVRRFCKCPVQAEADRVSSVYVTRSTGQEVSA 352

```

RESULT 11
Q6WN96 PRELIMINARY; PRT; 352 AA.
ID AC Q6WN96 STANDARD; PRT; 352 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE CC chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN Name=CCR5; Synonyms=CMKR5;
OS Cercobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecinae; Cercopithecidae;
OX NCBI_TaxID=9531;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=085, 087, 089, and Isolate 079;
RX MEDLINE=98321155; PubMed=9656999; DOI=10.1006/viro.1998.9174;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVem isolates use the CCR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage of
RL primary SIVem, HIV-2, and SIVmac.";
RL Virology 246:113-124(1998).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY278747; AAQ20015.1; -
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; -
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCRHOODOPS.
DR PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40458 MW; 0B4EA1B37CF16D90 CRC64;

Query Match 72.5%; Score 1377; DB 2; Length 352;
Best Local Similarity 75.2%; Pred. No. 3e-77;
Matches 258; Conservative 32; Mismatches 47; Indels 6; Gaps 2;

QY 24 FDYDYG--PCHKFDVKQIGQALLPPLYSLVFIFGVGNMLVLLINCKKLCITDIYL 81
DB 10 YDIDYGASEPCRKIDVKQGAHLLPPLYSWVFLFGVGNMLVLLINCKPKSMIDYIL 69
QY 82 LNLAISDLLFLITPLMAHSAANWVFGNAMCKLFTGLYHYGYFGGIFPIILLITIDRYLA 141
DB 70 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTWCQFLTGLYFGFGIFPIILLITIDRYLA 129
QY 142 IVHAVFALKARTVFGVTSVITWLVAVFASVPGIIFTKCKEBSVYVCGYFPRG---- 197
DB 130 IVHAVFALKARTVFGVTSVITWLVAVFASVPGIIFTRSQEGVHYTCSPHFPFGYQF 189
QY 198 WNNFHTIMRNITGLVLPILLIMVICYSGILKTLRCNKKRHRVRLFTIMIVVFLPWT 257
DB 190 WKNFEALKNWILGLVLPVLLVVICYSGILKTLRCNKKRHRVRLFTIMIVVFLPWA 249
QY 258 PYNIVILLNTQEFGLSNCSSTSLDQATQVETLGMTHCCINPIIVAFVGEKFRRLYS 317
DB 250 PYNIVILLNTQEFGLSNCSSTSLDQAMQVETLGMTHCCVNPPIIVAFVGEKFRYL 309
QY 318 VFRKHITRCKQCPVYFRTVDGVTSTNTPTSGEQRVSAGL 360
DB 310 VFRKHIAKCFERCISIFQKEAPERANSVYTRSTGEQISVGL 352

RESULT 12
CKR5_CERTO

```

FT VARIANT 107 L -> V (in isolate 089).  
FT VARIANT 134 V -> G (in isolate 079).  
FT VARIANT 146 V -> L (in isolate 085 and isolate 089).  
FT VARIANT 340 T -> I (in isolate 079).  
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;  
  
Query Match 72.4%; Score 1376; DB 1; Length 352;  
Best Local Similarity 76.4%; Pred. No. 3.5e-77;  
Matches 262; Conservative 31; Mismatches 44; Indels 6; Gaps 2;  
  
Qy 24 FDYDY--GAPCHKFDVKQIGAOQLPPLYSLVIFGFGVGNMLVLLINCKKLCCLTDIYL 81  
Db 10 YDIDYTTSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNILVLLINCKRLKSMTDIYL 69  
Qy 82 LNLAISSLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLIDRYLA 141  
Db 70 LNLAISSLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLIDRYLA 129  
Qy 142 IVHAFVFAKARTVTFGVVTSVITLWAVFASVPGIIFTKQKEDSVVCGPYFP---RG 197  
Db 130 IVHAFVFAKARTVTFGVVTSVITLWAVFASVPGIIFTRSQREGLHYTCSHPFPYQVQF 189  
Qy 198 WNNFHTIMRNILGLVPLLIWVICYSGLILKTLRCRNEKKHRAVRVIFTIMIVYFLFWT 257  
Db 190 WNFQTLKIVILGLVPLLVNVICYSGLILKTLRCRNEKKHRAVRVIFTIMIVYFLFWA 249  
Qy 258 PYNIVILLNTFQEPFGLNCSNCSQDQATQVTTGLMTHCCINPIIYAFVGEKFRYLS 317  
Db 250 PYNIVILLNTFQEPFGLNCSNCSNRLDQAMQVTTGLMTHCCINPIIYAFVGEKFRNYLL 309  
Qy 318 VFFRKHTKFCQCPVYRETVDGVTSTNTPSTGEQEVSAAGL 360  
Db 310 VFFQKHIAKFCCKCSIFQEQASERASSVYTRSTGEQEISVGL 352

RESULT 13  
Q71RS2 PRELIMINARY; PRT; 352 AA.  
AC Q71RS2  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Chemokine receptor CCR5.  
GN Name=CCR5;  
OS Cercocobus torquatus torquatus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Cercocobus.  
OX NCBI\_TaxID=81944;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21568355; PubMed=11711592;  
RX DOI=10.1126/JVI.75.24.12014-12027.2001;  
RA Beer B.E., Foley B.T., Kuiken C.L., Toozé Z., Goeken R.M., Brown C.R.,  
Hu J., St. Claire M., Korber B.T., Hirsch V.M.;  
RT "Characterization of novel simian immunodeficiency viruses from red-  
capped mangabeys from Nigeria (SIVrcmNG409 and -NG411).";  
RL J. Virol. 75:12014-12027(2001).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AF349682; AAK69684.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR002240; CC 5 receptor.  
DR InterPro; IPR000355; Chmkin receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00657; CCHEMOKINER.  
DR PRINTS; PR01110; CHEMOKINERS.  
DR PRINTS; PR00237; GPCRHHODOPSIN.

DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;  
  
Query Match 72.4%; Score 1376; DB 2; Length 352;  
Best Local Similarity 76.4%; Pred. No. 3.5e-77;  
Matches 262; Conservative 31; Mismatches 44; Indels 6; Gaps 2;  
  
Qy 24 FDYDY--GAPCHKFDVKQIGAOQLPPLYSLVIFGFGVGNMLVLLINCKKLCCLTDIYL 81  
Db 10 YDIDYTTSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNILVLLINCKRLKSMTDIYL 69  
Qy 82 LNLAISSLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLIDRYLA 141  
Db 70 LNLAISSLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLIDRYLA 129  
Qy 142 IVHAFVFAKARTVTFGVVTSVITLWAVFASVPGIIFTKQKEDSVVCGPYFP---RG 197  
Db 130 IVHAFVFAKARTVTFGVVTSVITLWAVFASVPGIIFTRSQREGLHYTCSHPFPYQVQF 189  
Qy 198 WNNFHTIMRNILGLVPLLIWVICYSGLILKTLRCRNEKKHRAVRVIFTIMIVYFLFWT 257  
Db 190 WNFQTLKIVILGLVPLLVNVICYSGLILKTLRCRNEKKHRAVRVIFTIMIVYFLFWA 249  
Qy 258 PYNIVILLNTFQEPFGLNCSNCSQDQATQVTTGLMTHCCINPIIYAFVGEKFRYLS 317  
Db 250 PYNIVILLNTFQEPFGLNCSNCSNRLDQAMQVTTGLMTHCCINPIIYAFVGEKFRNYLL 309  
Qy 318 VFFRKHTKFCQCPVYRETVDGVTSTNTPSTGEQEVSAAGL 360  
Db 310 VFFQKHIAKFCCKCSIFQEQASERASSVYTRSTGEQEISVGL 352

RESULT 14  
Q77776 PRELIMINARY; PRT; 352 AA.  
AC Q77776  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Chemokine receptor CCR5.  
GN Name=CCR5;  
OS Cercocobus torquatus torquatus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Cercocobus.  
OX NCBI\_TaxID=81944;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99059829; PubMed=9841919;  
RX Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M.S., Lu C.Y.,  
RA Aguilar R.F., Ho D.D., Marx P.A.;  
RT "Natural infection of a homozygous delta24 CCR5 red-capped mangabey  
with an Rb-tropic simian immunodeficiency virus.";  
RL J. Exp. Med. 188:2057-2065(1998).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AF084004; AAC62472.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR002240; CC 5 receptor.  
DR InterPro; IPR000355; Chmkin receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00657; CCHEMOKINER.  
DR PRINTS; PR01110; CHEMOKINERS.  
DR PRINTS; PR00237; GPCRHHODOPSIN.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.

KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 352 AA; 40475 MW; B3A63FDC4473DD1D3 CRC64;

Query Match 72.4%; Score 1375; DB 2; Length 352;  
Best Local Similarity 76.1%; Pred. No. 4e-77;  
Matches 261; Conservative 32; Mismatches 44; Indels 6; Gaps 2;

QY 24 FYDY--GAPCHKFDVKQIGALLPPLYSLSVIFGFGVGNMLVLLINCKLKCLTDIYL 81  
DB 10 YDIDYTSFPCQKINVKQIAARLLPPLYSLSVIFGFGVGNMLVLLINCKLKCLTDIYL 69  
QY 82 LNLAISSDLLFLTLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFPIIILLTDRYLA 141  
DB 70 LNLAISSDLLFLTLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFPIIILLTDRYLA 129  
QY 142 IVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTCKEDSVYVCGPYFP---RG 197  
DB 130 IVHAVFALKARTVTFGVVTSVITWVAVPASLPGIIFTSQREGLHYTCSPPHPSQYQF 189  
QY 198 WNNFTIMNLIQLVPLLIWVICYSGILKTLRCRNEKKRHRVAVPTIMIVVFLFWT 257  
DB 190 WNFOTLKIIVLGLVPLVWVICYSGILKTLRCRNEKKRHRVAVPTIMIVVFLFWA 249  
QY 258 PYNIVILLNTFOEPFGLSNCSTSDQATQVTTGLMTHCCINPIIYAFVGEKPRYLS 317  
DB 250 PYNIVILLNTFOEPFGLSNCSSNRDLQAMQVTTGLMTHCCINPIIYAFVGEKPRYLL 309  
QY 318 VFFRKHITKRCCKQCFVYFRETVDGVTSTNTPTSTGEQEVSAGL 360  
DB 310 VFFQKHIAKRCCKCSIFQKEAPERANSVYVTRSTGEQEISVGL 352

RESULT 15  
Q8H2T9 PRELIMINARY; PRT; 352 AA.  
AC Q8H2T9  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Chemokine receptor CCR5 (CC chemokine receptor 5).  
GN Name=ccr5;  
OS Saimiri sciureus (Common squirrel monkey).  
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
OX NCBI\_TaxID=9521;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22174698; PubMed=12186836;  
RA LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;  
RT "Blockade of HIV-1 infection of New World monkey cells occurs primarily at the stage of virus entry.";  
RL J. Exp. Med. 196;431-445(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,  
RA Seanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AF52615; AAN14531.1;  
DR EMBL; AY278742; AAQ20010.1;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.  
DR InterPro; IPR000923; BlueCu\_1.  
DR InterPro; IPR002240; CC\_5\_receptor.  
DR InterPro; IPR000355; Chmkin receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PRO00657; CCHEMOKINER.  
DR PRINTS; PRO1110; CHEMOKINER5.

DR PRINTS; PRO0237; GPCRHHODPSN.  
DR PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR 1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPTOR 2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 352 AA; 40542 MW; 9FC896FB7F074647 CRC64;

Query Match 72.4%; Score 1375; DB 2; Length 352;  
Best Local Similarity 75.2%; Pred. No. 4e-77;  
Matches 258; Conservative 32; Mismatches 47; Indels 6; Gaps 2;

QY 24 FYDYG--APCHKFDVKQIGALLPPLYSLSVIFGFGVGNMLVLLINCKLKCLTDIYL 81  
DB 10 YDIDYGPSEPCRKIDVKQKGAQLPPLYSLSVIFGFGVGNMLVLLINCKLKCLTDIYL 69  
QY 82 LNLAISSDLLFLTLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFPIIILLTDRYLA 141  
DB 70 LNLAISSDLLFLTLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFPIIILLTDRYLA 129  
QY 142 IVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTCKEDSVYVCGPYFP---RG 197  
DB 130 IVHAVFALKARTVTFGVVTSVITWVAVPASLPGIIFTSQKEGVHSCSPHPSQYRF 189  
QY 198 WNNFTIMNLIQLVPLLIWVICYSGILKTLRCRNEKKRHRVAVPTIMIVVFLFWT 257  
DB 190 WNFETLKNVILGLVPLVWVICYSGILKTLRCRNEKKRHRVAVPTIMIVVFLFWA 249  
QY 258 PYNIVILLNTFOEPFGLSNCSTSDQATQVTTGLMTHCCINPIIYAFVGEKPRYLS 317  
DB 250 PYNIVILLNTPDFFGVNCSNRDLQAMQVTTGLMTHCCINPIIYAFVGEKPRYLV 309  
QY 318 VFFRKHITKRCCKQCFVYFRETVDGVTSTNTPTSTGEQEVSAGL 360  
DB 310 IFFQKHIAKRCCKCSIFQKEAPERANSVYVTRSTGEQEISVGL 352

Search completed: June 9, 2005, 16:48:08  
Job time : 113.835 secs

**THIS PAGE LEFT BLANK**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:37:43 ; Search time 29.9183 Seconds  
(without alignments)  
898.236 Million cell updates/sec

Title: US-10-791-166-4  
Perfect score: 1900  
Sequence: 1 MLSTSRFRIRNTNSESVEV.....DGVTSNTPSTGQSVSAGL 360

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1900	100.0	360	1 US-08-450-393A-4	Sequence 4, Appli
2	1900	100.0	360	3 US-08-446-669-4	Sequence 4, Appli
3	1900	100.0	360	3 US-09-045-583-50	Sequence 50, Appl
4	1900	100.0	360	4 US-09-534-185-52	Sequence 50, Appl
5	1900	100.0	360	4 US-09-131-827A-2	Sequence 2, Appli
6	1900	100.0	360	4 US-09-625-573-4	Sequence 4, Appli
7	1900	100.0	360	5 PCT-US95-00476-4	Sequence 4, Appli
8	1900	100.0	377	4 US-09-949-016-11221	Sequence 11221, A
9	1899	99.9	360	4 US-09-131-827A-20	Sequence 20, Appl
10	1894	99.7	360	4 US-09-826-509-473	Sequence 473, App
11	1873	98.6	360	4 US-08-833-752-7	Sequence 7, Appli
12	1873	98.6	360	4 US-09-938-719-7	Sequence 7, Appli
13	1873	98.6	360	4 US-09-939-226B-7	Sequence 7, Appli
14	1849	97.3	360	3 US-09-045-583-51	Sequence 51, Appl
15	1849	97.3	360	4 US-09-534-185-51	Sequence 51, Appl
16	1838	96.7	347	1 US-08-461-244-3	Sequence 3, Appli
17	1651.5	86.9	374	1 US-08-450-393A-2	Sequence 2, Appli
18	1651.5	86.9	374	3 US-08-446-669-2	Sequence 2, Appli
19	1651.5	86.9	374	4 US-10-039-659A-14	Sequence 14, Appl
20	1651.5	86.9	374	4 US-09-625-573-2	Sequence 2, Appli
21	1651.5	86.9	374	5 PCT-US95-00476-2	Sequence 2, Appli
22	1651.5	86.9	387	4 US-09-949-016-11222	Sequence 11222, A
23	1568.5	82.6	344	3 US-08-466-343D-9	Sequence 9, Appli
24	1568.5	82.6	344	4 US-09-502-784A-9	Sequence 9, Appli
25	1473	77.5	329	4 US-09-502-783A-9	Sequence 9, Appli
26	1473	77.5	329	4 US-09-339-912A-9	Sequence 9, Appli
27	1473	77.5	329	4 US-09-195-662A-9	Sequence 9, Appli

28	1386	72.9	354	3 US-08-724-984A-2	Sequence 2, Appli
29	1371	72.2	352	3 US-09-517-605-5	Sequence 5, Appli
30	1370	72.1	352	3 US-09-045-583-52	Sequence 52, Appl
31	1370	72.1	352	4 US-09-534-185-52	Sequence 52, Appl
32	1364	71.8	352	3 US-09-087-232A-13	Sequence 13, Appl
33	1364	71.8	352	3 US-08-861-105-14	Sequence 14, Appl
34	1364	71.8	352	3 US-08-575-967A-2	Sequence 2, Appli
35	1364	71.8	352	4 US-08-833-752-5	Sequence 5, Appli
36	1364	71.8	352	4 US-09-796-202-1	Sequence 1, Appli
37	1364	71.8	352	4 US-09-938-719-5	Sequence 5, Appli
38	1364	71.8	352	4 US-08-771-276-2	Sequence 2, Appli
39	1364	71.8	352	4 US-08-771-276-20	Sequence 20, Appl
40	1364	71.8	352	4 US-09-939-226B-5	Sequence 5, Appli
41	1358	71.5	352	4 US-09-826-509-477	Sequence 2, Appli
42	1356	71.4	352	4 US-09-502-783A-2	Sequence 2, Appli
43	1356	71.4	352	4 US-09-502-784A-2	Sequence 2, Appli
44	1356	71.4	352	4 US-09-339-912A-2	Sequence 2, Appli
45	1356	71.4	352	4 US-09-195-662A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-450-393A-4  
; Sequence 4, Application US/08450393A  
; Patent No. 5707815  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; APPLICANT: Coughlin, Shaun  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; TITLE OF INVENTION: PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306-2155  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,393A  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cserr, Luann  
; REGISTRATION NUMBER: 11,822  
; REFERENCE/DOCKET NUMBER: UCAL-237/02US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5165  
; TELEFAX: 415-8857-0663  
; TELEX: 380816CooleyPA  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-450-393A-4

Query Match 100.0%; Score 1900; DB 1; Length 360;  
Best Local Similarity 100.0%; Pred. No. 8.6e-151;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNSESVEVTFDYDGAPCHKFDVKQIGAOQLLPPLYSLVFIQGVGN 60  
DB 1 MLSTSRFRIRNTNSESVEVTFDYDGAPCHKFDVKQIGAOQLLPPLYSLVFIQGVGN 60

QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
DB 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTGVTSTVITLWVAVFASVPGIIFTK 180  
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTGVTSTVITLWVAVFASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPFPFGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240  
DB 181 CQKEDSVYVCGPFPFGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240  
QY 241 AVRVITIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
DB 241 AVRVITIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAVGKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPTSGQEVSAGL 360  
DB 301 NPIIYAVGKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPTSGQEVSAGL 360

## RESULT 2

US-08-446-669-4  
; Sequence 4, Application US/08446669  
; Patent No. 6132987  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; TITLE OF INVENTION: PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,669  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neeley, Richard  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: UCAL-237/01US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5000  
; TELEFAX: 415-857-0663  
; TELEX: 380816CooleyPA  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-446-669-4

Query Match 100.0%; Score 1900; DB 3; Length 360;  
Best Local Similarity 100.0%; Pred. No. 8.6e-151;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSIVTFIFGVGN 60  
DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSIVTFIFGVGN 60  
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

DB 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTGVTSTVITLWVAVFASVPGIIFTK 180  
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTGVTSTVITLWVAVFASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPFPFGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240  
DB 181 CQKEDSVYVCGPFPFGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240  
QY 241 AVRVITIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
DB 241 AVRVITIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAVGKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPTSGQEVSAGL 360  
DB 301 NPIIYAVGKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPTSGQEVSAGL 360

## RESULT 3

US-09-045-583-50  
; Sequence 50, Application US/09045583  
; Patent No. 6287805  
; GENERAL INFORMATION:  
; APPLICANT: Graham, Gerard J. et al.  
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/045,583  
; FILING DATE: 20-MAR-98  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: MNI-044  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-09-045-583-50

Query Match 100.0%; Score 1900; DB 3; Length 360;  
Best Local Similarity 100.0%; Pred. No. 8.6e-151;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSIVTFIFGVGN 60  
DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSIVTFIFGVGN 60  
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120  
DB 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

QY 121 HIGYGGIPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180  
DB 121 HIGYGGIPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180  
QY 181 CQKEDSVVCGPYPRGWNPHITMRNLTGLVPLLMVICVSGILKTLRCRNEKKHR 240  
DB 181 CQKEDSVVCGPYPRGWNPHITMRNLTGLVPLLMVICVSGILKTLRCRNEKKHR 240  
QY 241 AVRVIPTIMIVFLFTWTPYINIVILLNTFOEFGLSNCESTSOLDQATQVETLGMTHCCI 300  
DB 241 AVRVIPTIMIVFLFTWTPYINIVILLNTFOEFGLSNCESTSOLDQATQVETLGMTHCCI 300  
QY 301 NPITIAFVGEKFRRLYSVFFRKHTTKRCKQCPVYFRETVDGVTSTNTPSTGEQVSVAGL 360  
DB 301 NPITIAFVGEKFRRLYSVFFRKHTTKRCKQCPVYFRETVDGVTSTNTPSTGEQVSVAGL 360

## RESULT 4

US-09-534-185-50  
; Sequence 50, Application US/09534185  
; Patent No. 6403767  
; GENERAL INFORMATION:  
; APPLICANT: Graham, Gerard J. et al.  
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
; Heptahelical Receptor Superfamily and Uses  
; Therefor  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/534,185  
; FILING DATE: 24-Mar-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/045,583  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: MNI-044  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: amino acid  
; LENGTH: 360 amino acids  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-09-534-185-50

Query Match 100.0%; Score 1900; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 8.6e-151;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNESGEVTFDFDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIGVGN 60  
DB 1 MLSTSRFRIRNTNESGEVTFDFDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIGVGN 60  
QY 61 MLVVLILINCKKGLTDIYLLNLAIISDLLFLITPLWAHSAANEVFGNACKLFTGLY 120

DB 61 MLVVLILINCKKGLTDIYLLNLAIISDLLFLITPLWAHSAANEVFGNACKLFTGLY 120  
QY 121 HIGYGGIPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180  
DB 121 HIGYGGIPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180  
QY 181 CQKEDSVVCGPYPRGWNPHITMRNLTGLVPLLMVICVSGILKTLRCRNEKKHR 240  
DB 181 CQKEDSVVCGPYPRGWNPHITMRNLTGLVPLLMVICVSGILKTLRCRNEKKHR 240  
QY 241 AVRVIPTIMIVFLFTWTPYINIVILLNTFOEFGLSNCESTSOLDQATQVETLGMTHCCI 300  
DB 241 AVRVIPTIMIVFLFTWTPYINIVILLNTFOEFGLSNCESTSOLDQATQVETLGMTHCCI 300  
QY 301 NPITIAFVGEKFRRLYSVFFRKHTTKRCKQCPVYFRETVDGVTSTNTPSTGEQVSVAGL 360  
DB 301 NPITIAFVGEKFRRLYSVFFRKHTTKRCKQCPVYFRETVDGVTSTNTPSTGEQVSVAGL 360

## RESULT 5

US-09-131-827A-2  
; Sequence 2, Application US/09131827A  
; Patent No. 6500030  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Michael  
; APPLICANT: O'Brien, Stephen J.  
; APPLICANT: Smith, Michael  
; APPLICANT: Carrington, Mary  
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A  
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE  
; FILE REFERENCE: 14014.0333  
; CURRENT APPLICATION NUMBER: US/09/131.827A  
; CURRENT FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/055,659  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-131-827A-2

Query Match 100.0%; Score 1900; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 8.6e-151;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNESGEVTFDFDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIGVGN 60  
DB 1 MLSTSRFRIRNTNESGEVTFDFDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIGVGN 60  
QY 61 MLVVLILINCKKGLTDIYLLNLAIISDLLFLITPLWAHSAANEVFGNACKLFTGLY 120  
DB 61 MLVVLILINCKKGLTDIYLLNLAIISDLLFLITPLWAHSAANEVFGNACKLFTGLY 120  
QY 121 HIGYGGIPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180  
DB 121 HIGYGGIPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTK 180  
QY 181 CQKEDSVVCGPYPRGWNPHITMRNLTGLVPLLMVICVSGILKTLRCRNEKKHR 240  
DB 181 CQKEDSVVCGPYPRGWNPHITMRNLTGLVPLLMVICVSGILKTLRCRNEKKHR 240  
QY 241 AVRVIPTIMIVFLFTWTPYINIVILLNTFOEFGLSNCESTSOLDQATQVETLGMTHCCI 300  
DB 241 AVRVIPTIMIVFLFTWTPYINIVILLNTFOEFGLSNCESTSOLDQATQVETLGMTHCCI 300  
QY 301 NPITIAFVGEKFRRLYSVFFRKHTTKRCKQCPVYFRETVDGVTSTNTPSTGEQVSVAGL 360  
DB 301 NPITIAFVGEKFRRLYSVFFRKHTTKRCKQCPVYFRETVDGVTSTNTPSTGEQVSVAGL 360

## RESULT 6

US-09-625-573-4  
; Sequence 4, Application US/09625573  
; Patent No. 6730301  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; Coughlin, Shaun  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94308-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/625,573  
; FILING DATE: 25-Jul-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,669  
; FILING DATE: May 25, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neeley, Richard  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: UCAL-237/01US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5000  
; TELEFAX: 415-857-0663  
; TELEX: 380816COOLEYPA  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-625-573-4

Query Match 100.0%; Score 1900; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 8.6e-151;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLSTSRSRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGPGVN	60
DB	1	MLSTSRSRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGPGVN	60
QY	61	MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANWVFGNAMCKLFTGLY	120
DB	61	MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANWVFGNAMCKLFTGLY	120
QY	121	HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGWTSVITLWVAVPASVPGIIFTK	180
DB	121	HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGWTSVITLWVAVPASVPGIIFTK	180
QY	181	CQKEDSVYVCGPFPFRGNWNNFTIMRNILGLVPLLIIMVICYSGILKTLRCRNEKKRHR	240
DB	181	CQKEDSVYVCGPFPFRGNWNNFTIMRNILGLVPLLIIMVICYSGILKTLRCRNEKKRHR	240
QY	241	AVRVIPTIMIVFLFWTPPNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI	300
DB	241	AVRVIPTIMIVFLFWTPPNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI	300
QY	301	NPIIYAFVGEKFRRLYSVFFRKHITKRCQCPVFRVRETVDGVTSTNTPTSGQEVSAGL	360
DB	301	NPIIYAFVGEKFRRLYSVFFRKHITKRCQCPVFRVRETVDGVTSTNTPTSGQEVSAGL	360

## RESULT 8

US-09-949-016-11221

## RESULT 7

PCT-US95-00476-4  
; Sequence 4, Application PC/TUS9500476  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Robbins, Berliner & Carson  
; STREET: 201 N. Figueroa Street, 5th Floor  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90012-2628  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00476  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berliner, Robert  
; REGISTRATION NUMBER: 20,121  
; REFERENCE/DOCKET NUMBER: 5555-291  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 310-977-1001  
; TELEFAX: 310-977-1003  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-00476-4

Query Match 100.0%; Score 1900; DB 5; Length 360;  
Best Local Similarity 100.0%; Pred. No. 8.6e-151;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLSTSRSRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGPGVN	60
DB	1	MLSTSRSRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGPGVN	60
QY	61	MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANWVFGNAMCKLFTGLY	120
DB	61	MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANWVFGNAMCKLFTGLY	120
QY	121	HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGWTSVITLWVAVPASVPGIIFTK	180
DB	121	HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGWTSVITLWVAVPASVPGIIFTK	180
QY	181	CQKEDSVYVCGPFPFRGNWNNFTIMRNILGLVPLLIIMVICYSGILKTLRCRNEKKRHR	240
DB	181	CQKEDSVYVCGPFPFRGNWNNFTIMRNILGLVPLLIIMVICYSGILKTLRCRNEKKRHR	240
QY	241	AVRVIPTIMIVFLFWTPPNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI	300
DB	241	AVRVIPTIMIVFLFWTPPNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI	300
QY	301	NPIIYAFVGEKFRRLYSVFFRKHITKRCQCPVFRVRETVDGVTSTNTPTSGQEVSAGL	360
DB	301	NPIIYAFVGEKFRRLYSVFFRKHITKRCQCPVFRVRETVDGVTSTNTPTSGQEVSAGL	360

```
; Sequence 11221, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11221
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11221

Query Match      100.0%; Score 1900; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 9.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
Db 18 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 77
Qy 61 MLVVLILINCKKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 78 MLVVLILINCKKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 137
Qy 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180
Db 138 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 197
Qy 181 COKEDSVVCGPYPRGWNPHFTIMRNILGLVLLIMVICYSIGILKTLRCRNEKKRHR 240
Db 198 COKEDSVVCGPYPRGWNPHFTIMRNILGLVLLIMVICYSIGILKTLRCRNEKKRHR 257
Qy 241 AVRVIPTIMIVYFLWTPYNIIVILLNTFOEPFGLSNCESTSOLDQATQVTTGLMTHCCI 300
Db 258 AVRVIPTIMIVYFLWTPYNIIVILLNTFOEPFGLSNCESTSOLDQATQVTTGLMTHCCI 317
Qy 301 NPITIAFVGEKFRRLYSVFFRKHITKRFCKQCPVYFRETVDGVTSTNTPSTGEQVSAGL 360
Db 318 NPITIAFVGEKFRRLYSVFFRKHITKRFCKQCPVYFRETVDGVTSTNTPSTGEQVSAGL 377

RESULT 9
US-09-131-827A-20
; Sequence 20, Application US/09131827A
; Patent No. 660030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014, 0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
; US-09-131-827A-20

Query Match      99.9%; Score 1899; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 1e-150;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
Db 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
Qy 61 MLVVLILINCKKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180
Db 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180
Qy 181 COKEDSVVCGPYPRGWNPHFTIMRNILGLVLLIMVICYSIGILKTLRCRNEKKRHR 240
Db 181 COKEDSVVCGPYPRGWNPHFTIMRNILGLVLLIMVICYSIGILKTLRCRNEKKRHR 240
Qy 241 AVRVIPTIMIVYFLWTPYNIIVILLNTFOEPFGLSNCESTSOLDQATQVTTGLMTHCCI 300
Db 241 AVRVIPTIMIVYFLWTPYNIIVILLNTFOEPFGLSNCESTSOLDQATQVTTGLMTHCCI 300
Qy 301 NPITIAFVGEKFRRLYSVFFRKHITKRFCKQCPVYFRETVDGVTSTNTPSTGEQVSAGL 360
Db 301 NPITIAFVGEKFRRLYSVFFRKHITKRFCKQCPVYFRETVDGVTSTNTPSTGEQVSAGL 360

RESULT 10
US-09-826-509-473
; Sequence 473, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 473
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-826-509-473

Query Match      99.7%; Score 1894; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 2.7e-150;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
Db 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
Qy 61 MLVVLILINCKKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180
Db 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180
```

QY 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCNEKKRHR 240  
DB 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
DB 241 AKRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360  
DB 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360  
RESULT 11  
US-08-833-752-7  
; Sequence 7, Application US/08833752  
; Patent No. 6448375  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; PARMENTIER, MARC  
; VASSART, GILBERT  
; APPLICANT: VASSART, GILBERT  
; APPLICANT: LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/833,752  
; FILING DATE: 9-APR-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6448375e  
US-08-833-752-7  
Query Match 98.6%; Score 1873; DB 4; Length 360;  
Best Local Similarity 98.3%; Pred. No. 1.5e-148;  
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNSESVEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLXSLVFIQFVGN 60  
DB 1 MLSTSRFRIRNTNSESVEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLXSLVFIQFVGN 60  
QY 61 MLVLLILNCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120  
DB 61 MLVLLILNCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFIIILLTDIYLAIVHAFKARTVTFGVTSVITLWVAVFASVPGIIFTK 180  
DB 121 HIGYFGGIFIIILLTDIYLAIVHAFKARTVTFGVTSVITLWVAVFASVPGIIFTK 180  
QY 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCNEKKRHR 240  
DB 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCNEKKRHR 240

QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360  
DB 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360  
RESULT 12  
US-09-938-719-7  
; Sequence 7, Application US/09938719  
; Patent No. 6692938  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; PARMENTIER, MARC  
; VASSART, GILBERT  
; LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/938,719  
; FILING DATE: 24-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/626,939  
; FILING DATE: 27-JULY-2000  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: <Unknown>  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6692938e  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-938-719-7  
Query Match 98.6%; Score 1873; DB 4; Length 360;  
Best Local Similarity 98.3%; Pred. No. 1.5e-148;  
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNSESVEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLXSLVFIQFVGN 60  
DB 1 MLSTSRFRIRNTNSESVEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLXSLVFIQFVGN 60  
QY 61 MLVLLILNCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120  
DB 61 MLVLLILNCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFIIILLTDIYLAIVHAFKARTVTFGVTSVITLWVAVFASVPGIIFTK 180  
DB 121 HIGYFGGIFIIILLTDIYLAIVHAFKARTVTFGVTSVITLWVAVFASVPGIIFTK 180  
QY 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCNEKKRHR 240

Db 181 CQKEDSVVCGPYPRGWNPHFIMRNILGLVLPILLIWIICYSGLIKTLRCNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSLDQAQVTTETLGMTHCCI 300  
 Db 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSLDQAQVTTETLGMTHCCI 300  
 QY 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFRETVDGVTSTNTPSTGQEVSAGL 360  
 Db 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 13  
 US-09-939-226B-7  
 ; Sequence 7, Application US/09939226B  
 ; Patent No. 6800447  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Euroscreen S.A.  
 ; APPLICANT: SAMSON, Michel  
 ; APPLICANT: PARMENTIER, Marc  
 ; APPLICANT: VASSART, Gilbert  
 ; APPLICANT: LIBERT, Frederick  
 ; TITLE OF INVENTION: Methods for Identifying Compounds which Bind the Active CCR5 Chem  
 ; TITLE OF INVENTION: Receptor  
 ; FILE REFERENCE: 9409/2023C  
 ; CURRENT APPLICATION NUMBER: US/09/939,226B  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: US 08/833,752  
 ; PRIOR FILING DATE: 1997-04-09  
 ; PRIOR APPLICATION NUMBER: US 09/626,939  
 ; PRIOR FILING DATE: 2000-07-27  
 ; PRIOR APPLICATION NUMBER: US 08/810,028  
 ; PRIOR FILING DATE: 1997-03-04  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 360  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: MISC FEATURE  
 ; LOCATION: (325)..(327)  
 ; OTHER INFORMATION: Xaa = any amino acid  
 US-09-939-226B-7

Query Match 98.6%; Score 1873; DB 4; Length 360;  
 Best Local Similarity 98.3%; Pred. No. 1.5e-148;  
 Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSILVFIQFVGN 60  
 Db 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSILVFIQFVGN 60  
 QY 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120  
 Db 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120  
 QY 121 HIGVFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180  
 Db 121 HIGVFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180  
 QY 181 CQKEDSVVCGPYPRGWNPHFIMRNILGLVLPILLIWIICYSGLIKTLRCNEKKRHR 240  
 Db 181 CQKEDSVVCGPYPRGWNPHFIMRNILGLVLPILLIWIICYSGLIKTLRCNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSLDQAQVTTETLGMTHCCI 300  
 Db 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSLDQAQVTTETLGMTHCCI 300  
 QY 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFRETVDGVTSTNTPSTGQEVSAGL 360  
 Db 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 14  
 US-09-045-583-51  
 ; Sequence 51, Application US/09045583  
 ; Patent No. 6287805  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Graham, Gerard J. et al.  
 ; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
 ; NUMBER OF SEQUENCES: 56  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/045,583  
 ; FILING DATE: 20-MAR-98  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mandragouras, Amy E.  
 ; REGISTRATION NUMBER: 36,207  
 ; REFERENCE/DOCKET NUMBER: MNI-044  
 ; TELEPHONE: (617)227-7400  
 ; TELEFAX: (617)742-4214  
 ; INFORMATION FOR SEQ ID NO: 51:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 360 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 US-09-045-583-51

Query Match 97.3%; Score 1849; DB 3; Length 360;  
 Best Local Similarity 97.2%; Pred. No. 1.5e-146;  
 Matches 350; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSILVFIQFVGN 60  
 Db 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSILVFIQFVGN 60  
 QY 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120  
 Db 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120  
 QY 121 HIGVFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180  
 Db 121 HIGVFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180  
 QY 181 CQKEDSVVCGPYPRGWNPHFIMRNILGLVLPILLIWIICYSGLIKTLRCNEKKRHR 240  
 Db 181 CQKEDSVVCGPYPRGWNPHFIMRNILGLVLPILLIWIICYSGLIKTLRCNEKKRHR 240  
 QY 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSLDQAQVTTETLGMTHCCI 300  
 Db 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSLDQAQVTTETLGMTHCCI 300  
 QY 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFRETVDGVTSTNTPSTGQEVSAGL 360  
 Db 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 15

US-09-534-185-51  
 ; Sequence 51, Application US/09534185  
 ; Patent No. 6403767  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Graham, Gerard J. et al.  
 ; TITLE OF INVENTION: No. 6403767ei Molecules of the G Protein-Coupled  
 ; Heptahelical Receptor Superfamily and Uses  
 ; Therefor  
 ;  
 ; NUMBER OF SEQUENCES: 56  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/534,185  
 ; FILING DATE: 24-Mar-2000  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/045,583  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mandragouras, Amy E.  
 ; REGISTRATION NUMBER: 36,207  
 ; REFERENCE/DOCKET NUMBER: MNI-044  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617)227-7400  
 ; TELEFAX: (617)742-4214  
 ; INFORMATION FOR SEQ ID NO: 51:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 360 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
 ;  
 ; US-09-534-185-51

Query Match 97.3%; Score 1849; DB 4; Length 360;  
 Best Local Similarity 97.2%; Pred. No. 1.5e-146;  
 Matches 350; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy	1	MLSTSRFRTRNTNESGEVTTFFDYDGAPCHKFDVKQIGALLPPLYSLVFIQFVGN	60
Db	1	MLSTSRFRTRNTNGSGEVTTFDDYDGAPCHKFDVKQIGALLPPLYSLVFIQFVGN	60
Qy	61	MLVVLILINCKKLCLETDIYLLNLAIISDLFLITPLMAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLSLTDIYLLNLAIISDLFLITPLMAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFPIILLTDIYLAIVHAFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK	180
Db	121	HIGYLGIGIFPIILLTDIYLAIVHAFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK	180
Qy	181	QKEDSVYVCGPYFPRGNWTFIMRNILGLVPLLIWICYSGLIKTLRCRNEKKRHR	240
Db	181	QKEDSVYICGPIFPRGNWTFIMRNILGLVPLLIWICYSGLIKTLRCRNEKKRHR	240
Qy	241	AVRVFTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI	300
Db	241	AVRLFTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTRQLDQATQVTTGLMTHCCI	300
Qy	301	NPITIVAVGKPRRYLSVFRPKHITKRCQCPVFRVETVDGVTSTNTPTSGEQVSAGL	360
Db	301	NPITIVAVGKPRRYLSMFFRKYITKRCQCPVFRVETVDGVTSTNTPTSGEQVSAGL	360

Search completed: June 9, 2005, 16:50:11  
 Job time : 30.9183 secs



Query Match	100.0%	Score 1900;	DB 9;	Length 360;
Best Local Similarity	100.0%;	Pred. No. 4.5e-150;		
Matches 360; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MLSTSRGRFRNTNNEESGEVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN	60	
Db	1	MLSTSRGRFRNTNNEESGEVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN	60	
Qy	61	MLVVLLINCKKLCITDIYLLNLAISDLFLITPLWAHSAANEWFGNAWCKLFTSLY	120	

```

Db      61  MLVVLILINCKKLCUCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY      121  HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWAVFASVPGIIFTK 180
Db      121  HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWAVFASVPGIIFTK 180
QY      181  CQKEDSVYVCGPYFPRGWNFNHIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
Db      181  CQKEDSVYVCGPYFPRGWNFNHIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
QY      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQFFGLSNCESTSLDQATQVTTETLGMTHCCI 300
Db      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQFFGLSNCESTSLDQATQVTTETLGMTHCCI 300
QY      301  NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
Db      301  NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 2
US-10-225-567A-460
; Sequence 460, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE OF INVENTION: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 460
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-460

```

```

Query Match      100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVIFGFGVGN 60
Db      1  MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVIFGFGVGN 60
QY      61  MLVVLILINCKKLCUCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
Db      61  MLVVLILINCKKLCUCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY      121  HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWAVFASVPGIIFTK 180
Db      121  HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWAVFASVPGIIFTK 180
QY      181  CQKEDSVYVCGPYFPRGWNFNHIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
Db      181  CQKEDSVYVCGPYFPRGWNFNHIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
QY      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQFFGLSNCESTSLDQATQVTTETLGMTHCCI 300
Db      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQFFGLSNCESTSLDQATQVTTETLGMTHCCI 300
QY      301  NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
Db      301  NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360

```

RESULT 3  
US-10-164-649-50

```

; Sequence 50, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/164,649
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-164-649-50

```

```

Query Match      100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVIFGFGVGN 60
Db      1  MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVIFGFGVGN 60
QY      61  MLVVLILINCKKLCUCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
Db      61  MLVVLILINCKKLCUCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY      121  HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWAVFASVPGIIFTK 180
Db      121  HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWAVFASVPGIIFTK 180
QY      181  CQKEDSVYVCGPYFPRGWNFNHIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
Db      181  CQKEDSVYVCGPYFPRGWNFNHIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
QY      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQFFGLSNCESTSLDQATQVTTETLGMTHCCI 300
Db      241  AVRVIPTIMIVYFLFWTPYNNIVILLNTFQFFGLSNCESTSLDQATQVTTETLGMTHCCI 300
QY      301  NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
Db      301  NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360

```

RESULT 4  
US-10-239-423-64

; Sequence 64, Application US/10239423  
; Publication No. US2003018689A1  
; GENERAL INFORMATION:  
; APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ADERMAN, Knut;  
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikola  
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the  
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammatory Cells and  
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,  
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine  
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction  
; FILE REFERENCE: 022217us  
; CURRENT APPLICATION NUMBER: US/10/239,423  
; CURRENT FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: DE10016013.1  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 64  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies  
US-10-239-423-64

Query Match 100.0%; Score 1900; DB 14; Length 360;  
Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRFRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLLPPLYSIVFIFGVGN 60  
DB 1 MLSTSRFRFRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLLPPLYSIVFIFGVGN 60  
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY 120  
DB 61 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY 120  
QY 121 HIGVFGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180  
DB 121 HIGVFGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGWNFNHIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240  
DB 181 CQKEDSVYVCGPYFPRGWNFNHIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300  
DB 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFFRKHTKFCQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360  
DB 301 NPIIYAFVGEKFRYLSVFFRKHTKFCQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360

## RESULT 5

US-10-439-845-8  
; Sequence 8, Application US/10439845  
; Publication No. US20030195348A1  
; GENERAL INFORMATION:  
; APPLICANT: Combatiere et al.,  
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS  
; TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/439,845  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 08/864,458  
; APPLICATION NUMBER: 08/864,458  
; FILING DATE: May 28, 1997  
; APPLICATION NUMBER: Provisional 60/018,508  
; FILING DATE: May 28, 1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 08830/030001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 8:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-10-439-845-8  
Query Match 100.0%; Score 1900; DB 14; Length 360;  
Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRFRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLLPPLYSIVFIFGVGN 60  
DB 1 MLSTSRFRFRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLLPPLYSIVFIFGVGN 60  
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY 120  
DB 61 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY 120  
QY 121 HIGVFGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180  
DB 121 HIGVFGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGWNFNHIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240  
DB 181 CQKEDSVYVCGPYFPRGWNFNHIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300  
DB 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFFRKHTKFCQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360  
DB 301 NPIIYAFVGEKFRYLSVFFRKHTKFCQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360

## RESULT 6

US-10-741-601-285  
; Sequence 285, Application US/10741601  
; Publication No. US20040166519A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001500  
; CURRENT APPLICATION NUMBER: US/10/741,601  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 26415  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 285  
; LENGTH: 360  
; TYPE: PRT

ORGANISM: Homo sapiens  
US-10-741-601-285

Query Match 100.0%; Score 1900; DB 16; Length 360;  
Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60  
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60  
QY 61 MLVVLILNCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120  
DB 61 MLVVLILNCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGWNPHITMRNIGLVPLIMVICYSGLIKTLRCNEKKRHR 240  
DB 181 CQKEDSVYVCGPYFPRGWNPHITMRNIGLVPLIMVICYSGLIKTLRCNEKKRHR 240  
QY 241 AVRVIETIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
DB 241 AVRVIETIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPSTGQEVSAAGL 360  
DB 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPSTGQEVSAAGL 360

RESULT 7  
US-10-741-601-286  
Sequence 286, Application US/10741601  
Publication No. US20040166519A1  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CL001500  
CURRENT APPLICATION NUMBER: US/10/741,601  
CURRENT FILING DATE: 2003-12-22  
NUMBER OF SEQ ID NOS: 26415  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 286  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-741-601-286

Query Match 100.0%; Score 1900; DB 16; Length 360;  
Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60  
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60  
QY 61 MLVVLILNCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120  
DB 61 MLVVLILNCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGWNPHITMRNIGLVPLIMVICYSGLIKTLRCNEKKRHR 240  
DB 181 CQKEDSVYVCGPYFPRGWNPHITMRNIGLVPLIMVICYSGLIKTLRCNEKKRHR 240  
QY 241 AVRVIETIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300

Db 241 AVRVIETIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPSTGQEVSAAGL 360  
Db 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPSTGQEVSAAGL 360

RESULT 8  
US-10-791-592-4  
Sequence 4, Application US/10791592  
Publication No. US20040219644A1  
GENERAL INFORMATION:  
APPLICANT: Charo, Israel  
Coughlin, Shaun  
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
PROTEIN RECEPTORS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
STREET: 5 Palo Alto Square  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306-2155  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/791,592  
FILING DATE: 01-Mar-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/625,573  
FILING DATE: 25-Jul-2000  
APPLICATION NUMBER: US/08/446,669  
FILING DATE: May 25, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Neeley, Richard  
REGISTRATION NUMBER: 30,092  
REFERENCE/DOCKET NUMBER: UCAL-237/01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-843-5000  
TELEFAX: 415-857-0663  
TELEX: 380816COOLEYPA  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-791-592-4

Query Match 100.0%; Score 1900; DB 16; Length 360;  
Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60  
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLPPLYSLVFIFGVGN 60  
QY 61 MLVVLILNCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120  
DB 61 MLVVLILNCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGWNPHITMRNIGLVPLIMVICYSGLIKTLRCNEKKRHR 240

Db 181 CQKEDSVVCGPYPRGNNFHTIMRNILGLVPLLLIMVICYSGLKTLRCRNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLFWPTPNVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300  
Db 241 AVRVIPTIMIVYFLFWPTPNVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAVGKPRYLSVFPKRIHTRKFCQCPVFFRETVDGVTSTNTPSTGQEVSAGL 360  
Db 301 NPIIYAVGKPRYLSVFPKRIHTRKFCQCPVFFRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 9

US-10-791-166-4  
; Sequence 4, Application US/10791166  
; Publication No. US20040223968A1  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10791,166  
; FILING DATE: 01-Mar-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/625,573  
; FILING DATE: 25-Jul-2000  
; APPLICATION NUMBER: US/08/446,669  
; FILING DATE: May 25, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neeley, Richard  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: UCAL-237/01US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5000  
; TELEFAX: 415-857-0663  
; TELEX: 380816COOLEYPA  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-791-166-4

Query Match 100.0%; Score 1900; DB 16; Length 360;  
Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSILVIFGVGN 60  
Db 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSILVIFGVGN 60  
QY 61 MLVVILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120  
Db 61 MLVVILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180

Db 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180  
QY 181 CQKEDSVVCGPYPRGNNFHTIMRNILGLVPLLLIMVICYSGLKTLRCRNEKKRHR 240  
Db 181 CQKEDSVVCGPYPRGNNFHTIMRNILGLVPLLLIMVICYSGLKTLRCRNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLFWPTPNVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300  
Db 241 AVRVIPTIMIVYFLFWPTPNVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAVGKPRYLSVFPKRIHTRKFCQCPVFFRETVDGVTSTNTPSTGQEVSAGL 360  
Db 301 NPIIYAVGKPRYLSVFPKRIHTRKFCQCPVFFRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 10

US-10-700-313-8  
; Sequence 8, Application US/10700313  
; Publication No. US20040259785A1  
; GENERAL INFORMATION:  
; APPLICANT: Combadiere et al.,  
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10700,313  
; FILING DATE: 31-Oct-2003  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/864,458  
; FILING DATE: 28-May-1997  
; APPLICATION NUMBER: Provisional 60/018,508  
; FILING DATE: May 28, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 08830/030001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-700-313-8

Query Match 100.0%; Score 1900; DB 16; Length 360;  
Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSILVIFGVGN 60  
Db 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSILVIFGVGN 60  
QY 61 MLVVILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120  
Db 61 MLVVILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180

Db 121 HIGYFGGIFPIILLTDRYLAIHVAHFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCNEKKRHR 240  
Db 181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCI 300  
Db 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCI 300  
QY 301 NPIIYAFVGEKPRYLSVFFPRKHITKRFCKQCPVFFRETVDGVTSTNTPSTGQEVSAAGL 360  
Db 301 NPIIYAFVGEKPRYLSVFFPRKHITKRFCKQCPVFFRETVDGVTSTNTPSTGQEVSAAGL 360

RESULT 11  
US-10-486-471-4  
; Sequence 4, Application US/10486471  
; Publication No. US20050101530A1  
; GENERAL INFORMATION:  
; APPLICANT: TOPIGEN PHARMACEUTIQUE INC.  
; TITLE OF INVENTION: CELLULAR VIRUS RECEPTORS AND METHODS OF USE  
; FILE REFERENCE: 00953-0003  
; CURRENT APPLICATION NUMBER: US/10/486,471  
; CURRENT FILING DATE: 2004-02-10  
; PRIOR APPLICATION NUMBER: U.S. 60/311,088  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-486-471-4

Query Match 100.0%; Score 1900; DB 17; Length 360;  
Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60  
Db 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60  
QY 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
Db 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTDRYLAIHVAHFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180  
Db 121 HIGYFGGIFPIILLTDRYLAIHVAHFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCNEKKRHR 240  
Db 181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCI 300  
Db 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCI 300  
QY 301 NPIIYAFVGEKPRYLSVFFPRKHITKRFCKQCPVFFRETVDGVTSTNTPSTGQEVSAAGL 360  
Db 301 NPIIYAFVGEKPRYLSVFFPRKHITKRFCKQCPVFFRETVDGVTSTNTPSTGQEVSAAGL 360

RESULT 12  
US-10-846-185-8  
; Sequence 8, Application US/10846185  
; Publication No. US20050118677A1  
; GENERAL INFORMATION:  
; APPLICANT: Combadiere et al.,  
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS  
; NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/846,185  
FILING DATE: 14-May-2004  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/864,458  
FILING DATE: May 28, 1997  
APPLICATION NUMBER: Provisional 60/018,508  
FILING DATE: May 28, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Halle, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 08830/030001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-846-185-8

Query Match 100.0%; Score 1900; DB 17; Length 360;  
Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60  
Db 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60  
QY 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
Db 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTDRYLAIHVAHFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180  
Db 121 HIGYFGGIFPIILLTDRYLAIHVAHFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCNEKKRHR 240  
Db 181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCNEKKRHR 240  
QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCI 300  
Db 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCI 300  
QY 301 NPIIYAFVGEKPRYLSVFFPRKHITKRFCKQCPVFFRETVDGVTSTNTPSTGQEVSAAGL 360  
Db 301 NPIIYAFVGEKPRYLSVFFPRKHITKRFCKQCPVFFRETVDGVTSTNTPSTGQEVSAAGL 360

RESULT 13  
US-09-131-827A-20  
; Sequence 20, Application US/09131827A  
; Patent No. US20020038469A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Michael  
; APPLICANT: O'Brien, Stephen J.

```

; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131.827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-20

Query Match          99.9%; Score 1899; DB 9; Length 360;
Best Local Similarity 99.7%; Pred. No. 5.4e-150;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
DB 1 MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLMAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLMAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPRGWNFNHTIMRNILGLVPLLMVLCYSGILKTLRCNEKKRHR 240
DB 181 CQKEDSVYVCGPYPRGWNFNHTIMRNILGLVPLLMVLCYSGILKTLRCNEKKRHR 240
QY 241 AVRVFTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
DB 241 AVRVFTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGGKPRYLSVPRKHIKTRFCQCPVYRETVDGVTSTNTPTSGEQEVSAGL 360
DB 301 NPIIYAFVGGKPRYLSVPRKHIKTRFCQCPVYRETVDGVTSTNTPTSGEQEVSAGL 360

RESULT 14
US-09-826-509-473
; Sequence 473, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 473
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-473

Query Match          99.7%; Score 1894; DB 10; Length 360;
Best Local Similarity 99.7%; Pred. No. 1.4e-149;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
DB 1 MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLMAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLMAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPRGWNFNHTIMRNILGLVPLLMVLCYSGILKTLRCNEKKRHR 240
DB 181 CQKEDSVYVCGPYPRGWNFNHTIMRNILGLVPLLMVLCYSGILKTLRCNEKKRHR 240

US-09-826-509-473

```

```

Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
DB 1 MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLMAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLMAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPRGWNFNHTIMRNILGLVPLLMVLCYSGILKTLRCNEKKRHR 240
DB 181 CQKEDSVYVCGPYPRGWNFNHTIMRNILGLVPLLMVLCYSGILKTLRCNEKKRHR 240
QY 241 AVRVFTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
DB 241 AVRVFTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGGKPRYLSVPRKHIKTRFCQCPVYRETVDGVTSTNTPTSGEQEVSAGL 360
DB 301 NPIIYAFVGGKPRYLSVPRKHIKTRFCQCPVYRETVDGVTSTNTPTSGEQEVSAGL 360

RESULT 15
US-10-925-095-473
; Sequence 473, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 473
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-925-095-473

Query Match          99.7%; Score 1894; DB 17; Length 360;
Best Local Similarity 99.7%; Pred. No. 1.4e-149;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
DB 1 MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLMAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLMAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPRGWNFNHTIMRNILGLVPLLMVLCYSGILKTLRCNEKKRHR 240
DB 181 CQKEDSVYVCGPYPRGWNFNHTIMRNILGLVPLLMVLCYSGILKTLRCNEKKRHR 240

US-10-925-095-473

```

